131 5.5 337 1 STAA_WOUSE P54/51 124 5.2 380 1 ST8C_MOUSE Q46689 123.5 5.2 381 1 STAA_PTG Q92745 119 5.0 359 1 STAA_MOUSE 088829	011206 092184 042173 0646877 09unp4 094239	110 4.6 566 1 SITA_CHICK 092183 109.5 4.6 573 1 SITA_CHICK PY0277 106.5 4.6 500 1 SITA_CHICK Q9ssc77 106 4.4 356 1 SITA_CHICKN Q9ssc77 106 4.4 356 1 SITA_CHICKN Q92185	103 6.4 3 374 1 SIZIBLONGAN 070137 103 6.2 3 375 1 SIZIBLONGAN 070137 100 4.2 375 1 SIZIBLONGAN 070237 100 4.2 375 1 SIZIBLONGAN 070397 92.5 4.1 6.5 1 GGAS-ZENEY 070397 92.5 3.9 759 1 PEROL-DRAW 070397	92 3.9 389 1 ECKS_MOUSE 092287 92 3.9 1877 1 ECKS_MOUSE 094592 89,5 3.8 712 1 S21E_HURAN 09704D5 89,5 3.8 2262 1 SAN_RABIT F57999		. SINGMEDIALS	STOCHART STANDARD PRP; 315 AA.		AS 127 SECTION N.A. SECTION N.A					CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC ox send an email to license@isb-sib.ch).
Georgian (c) 1993 - 2003 Compusen Itd.	OM nucleic - protein search, using frame_plus_nJp model. Run on: September 12, 2003, 16:2014 ; Search time 19:5 Seconds \$301.38 Million ccl. updaces/sec	File: 0S-09-714-936-218 Particle sore: 238 Segumes: 1 coggamaticoggicagestttcttctccttttttttg 1294 Segumes:	Scortag table: gL/SSD/62 Napop 10.0 Napsert 0.5 Napop 10.0 Yelecer 0.5 Papop 6.0 Pelacer 7.0 Papop 6.0 Pelacer 7.0	Searched: 127863 seqs, 47026705 residues Total number of hits satisfying chosen parameters: 255726	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100 Listing first 43 summaries	Command, line patraceter; 1.	Database : SwissProt_41:*	Pred. No. is the number of results predicted by chance to have a soon of a product of the tenth being printed, and referred by handy layers of the tenth being printed, and fairthy by markets of the consequent statement.	Smealt 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	941 39.5 305 1 SITC_RAY 064686 917 38.5 305 1 SITC_MOUSE 094wr2 415 17.4 36.0 1 SITD_MOUSE 0922b6 382 16.0 302 1 SITD_HUMAN 0914611	238.5 13.8 346 15/7E_DONAN QOPUNT 319.5 13.4 336 15/7E_DONSE QOSGY11 165 6.8 413 1 STAL_CHICK QOSJ82 146.5 6.1 463 1 STAL_CHICKS QOSG88 146.5 6.0 406 1 STAL_CHICKS QOSG88	5 8 474 1 STAND MAT 1971 1971 1971 1971 1971 1971 1971 197	134 5.6

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81 AlaValSerAsnSerGlyGlnMetValGlyGlnLysValGlyGluGluIleAspArg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586 GATTATTTTTCGAAGGGAAGCGAATACTACTATTTGTGTTAGTTGGGGACCTTTCGGCAAT 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 MethrgIysAspGlyAsnGlyIleValTyrAsnMetLeuLysLysThrValAspAlaTyr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             706 CCGAATGCCCAAATATACGTGACCACAGAGAAGCGCATGAGTTACTGTGAGGGTTTTT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ProAspAlaGluIleTyrValThrThrGluGlnArgMetThrTyrCysAspGlyValPhe 200
                                                                                                                                                                                                                                                                                                                                                    166 ATGGCCTGCATCCTGAAGAGAAGTCTGTGATTGCTGTGAGGCTTCATAGCAGCGTTCCTT 225
                                                                                                                                                                                                                                                                                                                                                                                                             226 TTCCTGCTGGTTGTGGTCTTGTAAATGAAGTGAATTTCCCAFTGCTACTAAACTGCTTT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                  21 IeuLeullaMetArgleuAlaAsnAspValThrPheProLeuLeuAsnCysPhe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 CACTATGGATACATAAATGTGAAGACACAAAGAGCCTTTGCAACTGGACTGTGACCTTTGT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HistyrGlyTyrlleAsnValArqfbrGluGluProleuGluLeuAsnCysAsnHiscys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetalaCysIleLeuLysArgLysProAlaLeuAlaValSerPheIleAlaLeuCysIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCCTGCATTTGGAGAATGAACAATGCCCCCCCAAAGGTTATGAAGAAGATGTCGGC
                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
             EMEL, L29554, AAC42086.1; -.
LiterPro: IRROURTS, GlyCo_Lrans_29.
Pfam: PROUTTY, GlyCo_Lransf_29.
Transferase, GlyCosyLtransferase; GlyCoprotein: Transmembrane,
                                                                                                            (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
                                                                                                                                                                                   9077F6547D359AE9 CRC64:
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1173
0 0
                                                                                 CYTOPLASETC (POTENTIAL)
                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                   N-LINKED GLCNAC
                                                                                                                                                                                                                            Length:
Matches:
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                                                                 Signal-anchor; Golgi stack.
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91.35%
83.17%
39.49%
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305 AA;
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Query Match:
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Pred. No.:
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SI7C_MOUSE
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STANDARD;

Q9WUV2; Q9JHP5;

SI7C MOUSE

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wise STES STORY matry is opergright. It is produced through a cultibration between the Steas institute of Bioinformatics and the Wath operation on Its Burneau and Sofinformatic Institute. There are no restrictions on Its mass 178 and Profit institutions are long a first content of the Steas of the Stead of the Steas of the Steak of the Steak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TYPE-II MEMBRANE PROTEIN)

    -1- DEVELORMENTAL STAGE: IN BRAIN, EXPRESSION REACHES MAXIMUM LEVELS
AT DAT 12 OF THE DEMENDING STAGE, KEEPS ALMOST SIMILIAR LEVELS
DURING MOUSE DEVELORMENT.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I-FUNCTION: INVOLVED IN THE BIOSYMPHESIS OF GANGLIOSIDE GDIA FROM GRIAD. TRANSFRANCE TWO SALMANC. FRESIDES ON WERAC. 2.3 -GAL-BETA-1.3 -GALANC. OF GIXCOPROFEINS AND GLYCOLIPPIDS. SPÉGALMACLII PREFERS GLYCOLIPPIDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO A LESSER EXTENT IN KIDNEY, MAMMARY GLAND, SPLEEN, TESTIS AND
                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mushae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Přem. Př00777; Glyco_transf_29; I.
Transferase, Glycosyltransferase, Glycoprotein, Transmembrane;
28-TEB-2003 (Rel. 41, Created)
28-TEB-2003 (Rel. 41, Last sequence update)
28-TEB-2003 (Rel. 41, Last amoutation update)
Alphan-Veory)shalecocomminde alpha-2, 5-Stalytransferase III
(RC 24, 99-7) (GPGalMo III) (SJalytransferase 7C) (GPT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 29.
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LUMENAL, CATALITIC (POTENTIAL).
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EMBL, Y11343; CAB95031.1; --
EMBL, Y11344; CAB95031.1; JOINED.
EMBL, Y11345; CAB95031.1; JOINED.
EMBL, Y11346; CAB95031.1; JOINED.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOPROFEINS.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nu	ON nucleic - pucleic search, using sw mode)
Run on:	September 12, 2003, 12:38:03; search time 5026 Seconds (without alignments) 10352.642 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-714-938-218 1294 1 coggasticocggglogacgttbcttctccttttttg 1294
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 seqs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0	Minimum DB seq length: 0 Maximum DB seq length: 20004000000

Post-processing: Minimum Match 09 Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

	gb_ba:*	Jb_htg:*	pp_in:*	th_om:*	*: ^o qt	fb pat:*	*: td di	qp_p1:*	tb_pr:*	qb_ro:*	qb_sts:*	4: AS QD	dp nu:*	qb_v1:*	em ba:*	em_fun:*	em_hum:*	em în:*	em_mu:*	em_om:*	em_or:*	em_ov:*	em_pat:*	em_ph:*	em_pl:*		em_sts:*	em_un:*		htg	em_htg_inv:*		htg		em htg rod:*		em_htg_vrt:*	en_sy:*	em_htgo_hum:*	em htdo mus:*
ñ.																	17:	18:	19:	30:	21:	35:	23:	24:	25:	26:	27:	38:	39:	30:	31:	35:	33:	34:	32:	36:	37:	38:	39:	40:

Pred. No. is the number of results predicted by chance to have a 40: em_htgo_mus:* 41: em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

No. Stock of the which length be Description 2 7.159 94.7 10.0 8.00	***						
1, 10, 10, 10, 10, 10, 10, 10, 10, 10,	2	8	Match	Length	8	A	
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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2	743	57.4	1106	φ	546	76468
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10 10 10 10 10 10 10 10	**	643	49.7		5		1 Homo
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ALIGNMENTS

RESULT 1

AK091215	
LOCUS	AK091215 3207 bp mRNA linear PRI 15-JUL-2002
DEFINITION	Homo sapiens cDNA FLJ33896 fis, clone CTONG2007959, highly similar
	to ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2, 6-SIALTLERANSFERASE (EC
	2.4.99).
ACCESSION	AK091215
VERSION	AK091215.1 GI:21749532
KEYWORDS	oligo capping; fis (full insert sequence).
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
	Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
REFERENCE	
ATTENDES	ATTHORS Nishir Otar Nakadawa C Conch. a Misumochi H Transki u

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PAT 01-MAR-2002
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988 CIGGACIGIGACCITIGRECOLARGICACAACICAGGICAGATGGCTGGCCAGAAGGTG 447
                                                                            371 CTGGACTGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGAAGGTG 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 GGAAAIGAGAIAGAICGAICCICCIGCAITIGGAGAAIGAACAAIGCCCCCCAACAAAGGI
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Gurney,A.L., Pan,J., Smith,V., Matanabe,C.K., Wood,W.I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia: Butheria: Primates: Catarrhini: Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 TACTGTGATGGAGTTTTTAAGAAGGAAACTGGGAAGGACAGAGTCCA 777
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Genentech, Inc. (US)
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Sequence 535 from Patent WOU16848.
AX376468
AX376468.1 G1:19170623
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/db_xref="taxon:9606"
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Vandence A., routel, r. stor. Benkinsen A., rainis.

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Vandence A., radaris, r. stor. V. Satien, V. Satien, V. Resten, V. Satien, V. Resten, R. Res
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MRKDGNGI I YNMLKKTVGIY PNAQIIYYTTRKRASYCDGVFRKRETGKDRVOSGSYLSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPTPLLAMDACYGIHVYGMINDTYCKTEGYRKVPYHYYEQGRDECDEYFLHEHAPYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICATA GOAGOGIT COTTITICOTGOTGOTGOTGOTT COTA ANGRA ANGRA ANTOCOTA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GAGGGCGGCGGCGGAGCGCCATGGCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTChiagcagcoffccttfffcctgctgctgctgctgtctfctaaatgaagtgaattfccca 267
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/dione_lib="crowa2"
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149. .1066
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/db_xref="taxon:9
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SeqDerXap

SeqDerMap FngrPrnt

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<800

1086 recorrenganacecaacercagetractrotrotrotrocrecercascreactracter 1146 ATGTGGCCTACCTCACATTGTTTGTTACACCTACACAGGAAAAAGGAAAATGTCCTT 1205 786 CAGGGGCCATGCAAGGCGACTGCTGATTTCTACAGACACTTTTTAAGCGATTACCAGTGC 845 846 FGGCAAGTGGAACTACCTTTCCGGTCCTTTACAAGCATCCAGTCACTTGCTGAAATGTC 905 906 ATAAGGGATATAAACCTGCTGACAGGCCAGGATCATTGCATCTCCTGCTGCTTCTA 965 Gaps ö Length 104714; 0; Indels Query Match
39.3%; Score 508; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 6.5e-128;
Actholes 508; Conservative 0; Mismatches 0; g g à ä a Ž, à 음 à a <800 <800

1206 TTGRATICCATGCTTGTAGAGATGTJCATCCAATTTGAATGAACATGTAGCCAAGGTAGTG 1265

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all regions were either double-stranded or agequaced with an alternate chemistry or covered by hish quality data (i.e., pixed quality >= 30). an attempt was made to resolve all sequencing problems, such as compressions and repeals; all replaces were covered by at least toe place and accompressions and repeals; all replaces were such as exercised quality and accompressions and repeals all replace were such as the second and accompressions and repeals all replace were such as assembly was confirmed by restriction digest.	Sequence Validation: This sequence has been validated by Multiple Complete Digest fingeritating Comperison of the experimentally derived digest fingeritating Comperison of the experimentally derived digest fragments with expensive predefet fingements at given below the deterrorieally digested sequence consists of both insert on the deterrorieally digested sequence consists of both insert on	vector, in order to accurately represent the entire circula Small framents below a variable cutoff (approximately 400- are not resolved in the fingerprint and hence do not appear	to the table. There ear to significant remaining distributions between the experimental and predicted values in fragments are separated by dashed lines at the significant of the significant in the significant of the signif	SegDerMap Engibrnt SegDerMap EngiPrnt SegDerMap EngiPrnt	2673 2656 8696 8892 608 <800	2097	9310 9448 1130 1103 512 <800	4847 4729 355 <800 449 <800	7893 7784 2766 2720 4126 4148	2507 2533 10733 10597 2736 2734	2129 2097 267 <800 1050 1046	391 <800 10200 10171 4537 4464	376 <800 6463 6472 1432 1383	316 <800 2429 2496 4442 4464	490 <800 5709 5523 4880 4916	1018 1040 124 <800 1388 1383	6659 6772 1914 1931 2955 3001	1662 1597 7949 8005 14155 14162	255 <800 2512 2496 5281 5243	1163 1141 4071 4041 2155 2159	857 902 2482 2496 3968 3968	33 <800 5597 5523 4023 3968	2827 2821 1415 1414 1035 1046	14622 14353 74 <800 2123 2099	902 906 923 2130 2159	7619 7784 3697 3783 165 <800	1060 1040 1001 1012 349 <800	
	AC099672 16641 bp DNA 11sear PRI 30-NPR-2002 HOMO suptems chromosome 1 close RP11-286410, complete sequence.	AC099672 AC099672.2 GI:20340491 HTG.	MISM HOmo saptems (numan) NISM HGmo saptems explans Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mommalla, Butheria, Primates, Catarrhini, Hominidae, Bomo.	 (bases I to 166441) (Raul, R.K., Olson, W.V., Zhou, Y., James, R.A., Rouse, G., Mu, Z., Saephimmachak.C., Phelps, K.A., Buckley, D., Raymond, C., and 	Haugen, E.D. Direct Submission Impublished	2 (bases I to 166441) Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, B.D.	Direct Submission Submitted (17-NOV-2001) Genome Center, University of Washington,	Box 352145, Seattle, WA 98195, USA 3. (bases 1 to 166441)	<pre>RAUL, B.K., Ulson, B.V., Zhou, I., James S.R., Rouse, F., Wu, Z., Sachphigmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and France, B. D.</pre>	Daugethere. Direct Manigsion Submitted (30-200-2003) Canoma Caster Indusedity of Washington	Summitted (50-arx 2002) Genume Center, University of Mashington, Box 352145, Seattle WR 96195, USA	On Apr 20, 2002 Line Sequence Version repraced gricos/2014	Center Code: UNGC	NeD Site: nttp://www.gemonse.washington.edu Contact: uwgohings@u.washington.edu	Center project name: chr.1	Center clone name: RPLL-260H10 (SGU344)	Sequencing vector: plasmid; 93% of reads Sequencing vector: plasmid; 108752; 7% of reads	Chemistry: Dye-terminator Big Dye: 14% of reads	Assembly program: Phrap; Version 0.990319 Consensus quality: 166664 bases at least 040	Consensus quality: 16640 bases at least Q30 Consensus quality: 16641 bases at least Q20	insert size: recent; sum of contigs Quality coverage: 8.3x in Q20 bases; sum-of-contigs		3': MED-ILDSMIS (UNGU:SCUBBU) ACIUSZ/9, 960Ub-DD OVETIAD 3': Mapping in progress	Sequence Quality Assessment:	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	All manusly colled bases have been reduced to quality zero. Quality levels above 40 are expected to have less than	I write in 10,000 pp. Base-by-base quality values are not generally visible from the	GenBank flat file format but are available as part

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1112	339	3912	3412	5157	3802	1435	694	7139	4563	1946	3846	5381	443	2927	5478	448	2141	6411	2573	7241	2035	1241	4450	2587	2663	1089					lifiers	39.3%; Score 508; DB 9; L 100.0%; Pred. No. 6.6e-128; 3ye 0: Mismatches 0;	CTGCTGATTTCTA	UTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
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11209	278	5913	250	724	7251	2080	3431	741	4138	291	3587	2506	731	6882	5282	2262	1475	545	3252	78	3192	3192	522	2580	903	3470	6419	2595	6322	2808	FEATURES	Query Match 39.3 Best Local Similarity 100. Matches 508: Conservative	786	Db 59102 CAGGGGGCARGCGAAGGCGACTGCTGATTCTACAGACACTTTTAAGCGATTACCAGTGCT 59161

Chemistry: Dye-terminator E7; 94% of reads Chemistry: Dye-terminator E8; Dyes, 6% of reads Assembly program: Phrap; version 0,990319	sensus quality: 191831 bases at least 040 sensus quality: 191959 bases at least 030	nsensus quality: 191976 bases at least 020	whity coverage: 8.5x in Q20 bases; sun-of-contigs
Chemistry Chemistry Assembly	Consensus	Consensus	Quality co

Overlapping Sequences: 5': RE5-829Ds AL138797 3': RE5-963MS (UNGC:sc0227) AC099769, 72727-bp overlap

This entry has been amorbted with sequence quality mission could be the managed with sequence quality fairsters computed by the heave assembly program.

All manually deliced bases have been reduced to quality seco. All manually deliced bases have been reduced to quality seco. The could be the second of a second of a second of a second base of the second of a second base of the country of the country of ANN 1 file.

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Dispulsable to 18685) Bitton B. Linco, L. Mensana, C., Lander, E., Alden, K., Anderson, M., Shariman, B., Linco, L., Septimiraty, E., Septimiraty, L., Bouchaller, J., Charles, M., Candina, C., Condina, C., Condin
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PETTERKYPRAGMAKRINTYFTEDRWID.*
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                                                              Mus musculus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Muridaa; Miritaae Mus
                                                                                                     Mammalia, Eutheria, Rodentia, Sciurognathi, Muridee, Murinae, Mus
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Dfemical, Research (RKRRN), Glyco Molecular Biology, Frontier
Research Program, Fako, Saitama 351-01, JAPAN
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                                                                                                                                            Lee, Y.C., Kaufmann, M., Kitazume-Kawaquchi, S., Kono, M.
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Pred. No. 7e-112;
0; Mismatches 116; Indels
                   GalNAc alpha-2, 6-sialvitransferase III.
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                                       Mus musculus (house mouse)
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               /clone_lib="RPCI-11 Buman Male BAC"
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Pred. No. 1.8e-127;
0; Mismatches 1;
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12663. .23766
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Page 12

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3373	2397	6	979	177	7	1848	6207	2599	1346	1004	543	1893	10227	910	1156	3009	6303	8937	2764	2969	2050	585	4282	3257	5452	1910	793	9342	1729	5936	3149	2199	2758	lifiers	 .99680 /organism~"Homo sapiens" 	/mol_type="genomic DNA"
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69	1554	1774	3209	1674	15633	2149	2439	1743	4996	198	2289	4347	1336	1096	5165	3234	12762	1160	286	1446	2883	2114	09	1797	464	3102	364	6320	2899					100	.; ©	/mc
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ence version replace	Washington Genome C	genome.washington.ed	asimily contract	chr-1	5-963M5 (SC0227) tistics	asmid; 48% of reads asmid; LOB752; 52% o	ator ET; 82% of read ator Big Dye; 18% of	ap; version 0.990319 372 bases at least Q	651 bases at least Q 678 bases at least Q	um-of-contigs x in Q20 bases; sum-		ess C:sc0329) AC103592	nt:	tated with sequence e Phrap assembly pro	s have been reduced are expected to have	ues are not generall	. Dut are available a le.	d as follows unless	ouble-stranded or se wered by high qualit	t was made to resolv sions and repeats; s	lasmid subclone or m y was confirmed by n		alidated by Multiple on of the experiment	predicted fragments ted sequence consist	variable cutoff (app	no significant remai	by dashed lines.		SeqDerMap FngrPrnt				512 <800		1247 1215	4695 4684
On May 30, 2002 this sequence version replaced gi:17017968	Center: University of Washington Genome Center	Web site: http://www.genome.washington.edu	Drafting Center: SC	Center project name: chr-1	Center clone name: RP5-963M5 (sc0227)	Sequencing vector: pl Sequencing vector: pl.	Chemistry: Dye-terminator ET; 82% of reads Chemistry: Dye-terminator Big Dye; 18% of reads	Assembly program: Phr Consensus quality: 99.	Consensus quality: 99 Consensus quality: 99.	Insert size: 99680; sum-of-contigs Quality coverage: 7.1x in Q20 bases; sum-of-contigs	Overlapping Sequences:	5': Mapping in progress 3': RP11-335E14 (UNGC:sc0329) AC103592	equence Quality Assessme	fals entry has been anno estimates computed by th	All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than	1 error in 10,000 bp. Base-by-base quality values are not generally visible from the	GenBank flat file format bu of this entry's ASN.1 file.	This sequence was finished as follows unless otherwise noted:	all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred	uality >= 30); an attemproblems, such as compres	covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest	Sequence Validation:	This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived dig	Tragments with sequence predicted tragments is given below. The electronically-digested sequence consists of both insert and	Small fragments below a	in the table. There are	fragments are separated		SeqDerMap FugrPrnt Seq				8065 8256			7169 7251
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Assembly program, MX54', writind 4.5
Sequencing vector: plasmid; L0973. 1000 of reads
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Combinativ; playerinator page 1999; 1000 of reads
Consensus quality; 12554 bases t. Less 0.0
Consensus quality; 12554 bases t. Less 0.0
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runs of N, but the exact sizes of the gape are unknown. 
This record will be updated with the finished sequence 
as soon as it is available and the accession number will 
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2211. conclig of 2241 bp in length
11222 conclig of 2822 bp in length
11232 conclig of 6822 bp in length
11232 conclig of 6822 bp in length
54059 conclig of 64557 bp in length
64241 contig of 7272 bp in length
64281 contig of 7273 bp in length
64281 contig of 7273 bp in length
64281 contig of 7273 bp in length
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sqs of 1100 bp
contig of 20035 bp in length
sqs of 100 bp
contig of 8222 bp in length
gqs of 100 bp
contig of 8222 bp in length
sqs of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of 100 hp an length contig of 10481 bp in length gap of 100 hp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7058 bp in length
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/note="%ssembly_fragment:00383"
64364. .71431
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1532, ,82012
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/note="assembly_fragment:00577"
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1. .224
/note="assembly_fragment:00851
clone_end:SP6
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                     ---- Summary Statistics
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="RP4-800018"
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BOND Sepidens chromosome 1 close Re4-800D18, *** SEQUENTER IN
AL199155 **, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACTCAGGTGAATGGTTG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 GCCAGARGGTGGGAAATGAGATAGATCGTCCTGCATTTGGAGAATGAACAATGCCC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 CCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTCGAGTTGTGTCCCATA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         557 CCAGCGTTCCTCTTTTGCTAAAAACCCTGATTATTTTTTCAAGGAAGCGAATACTACTA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 TTIGTGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTTACA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 ACATGITGAAAAGACAGITGGIATCIATCGAATGCCCAAATAIACGIGACCACAGAGA 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (0.7072.2010) Sunger Centre, Rinxton, Cambridgeshize, CEIO 180, UR. Frantl enquirites: hunquery/esanger.ac.uk Clone request/esanger.ac.uk clone-request/esanger.ac.uk clone-request/esanger.ac.uk clone-request/esanger.ac.uk clone-request/esanger.ac.uk clone-request/esanger.ac.uk clone-request/esanger.ac.uk clone-request/esanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737 AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGGGG 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owery Match

31.8%; Score 411.8; DB 9; Length 99680;
Best Local Smilarity 9; S8; Pred. No. 1.66.10;
Matches 413; Conservative 0; Manaches 2; Indels 0;
                                                                      /close_lib="RPCI human PAC library 5"
                                                                                                                1...4

7.000-8.ingle subclore region*

7.001-8...3044

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Project Information
Center project name: dJ800D18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk
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                                          'clone-"RP5-963M5"
'chromosome-"1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL139155.3 GI:9212195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plumb, B.
                                                                                                                                                                                                                                                                                                                                                                                                        33193
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                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                        SASE COUNT
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Best Local Similarity:
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Mismatches:

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This STATES APPT entry is expectight. It is produced through a cultivocrtic between the Seiss institute of Michifornation and the BMB, outstation the Banceau the Shift State of Michifornation and the BMB, outstation use TV non-profit, institutions as loops as its content is in no way an expect, the michifornation as loops as its content is in no way entities expected a license accessed to Seiss and the Charles all includes accessed the Michigan Seiss and the Charles and the American Seiss and the Seiss accessed to Seiss and the Seiss and the Seiss accessed to Seiss and the Seiss and Seiss 
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PQRTPIRSF (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                        Taksshims S., Kurosawa N., Tachida Y., Inoue M., Tsuji S.;
Topparative analysis of the genomic structures and promoter
activities of mones Jslaz, Jenib, Jsaliko clalikoca, Jesiajitranse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
Neuko-alpha-2,3Gal-beta-1,3GalNAC-alpha2,6-sialyltransferase and anally, SFGalNAC-III and IV.*;
TyfGalNAC-III and IV.*;
Tyf.11958-11967(1399).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND COLON AND TO A LESSER EXTRAIT IN LUDA. HEARY, KINBRY, SPECIER AND THYROS.
-I- DEVELOREMENT, STAGE: DEVELOREMENTLY RESULATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110chem. 127:399-409(2000).
FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GANGLIOSIDE GDIA FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMIB. TRANSFERS CMF-NEUGC WITH AN ALPHA-2,5-LINKAGE TO GALNAC
RESIDES ON NEUDACA-ALPHA-2,3-GAL-BERT-1,3-GALMAC OF GENCOROTEINS
AND GLYCOLIFIDS. PREPRIS GLYCOPROTEINS TO GLYCOLIFIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAMBLYTIC ACTUVITY: CMP-N-acetylneuraminate + alpha-N-acetylneuraminy1-2,3-betx-D-galactosyl-1,3-W-acetyl-1-and-nyf-1,3-W-acetyl-1-and-nyf-1,3-W-acetyl-1-and-nyf-1,3-W-acetyl-neuraminy1-2,3-betx-0-galactosyl-1,3-(alpha-N-acetyl-auraminy1-2,3-betx-0-galactosyl-1,3-(alpha-N-acetyl-auraminy1-2,1,5-W-acetyl-1-a-and-nyf-1,1-alpha-N-acetyl-auraminy1-2,1,5-W-acetyl-1-a-and-nyf-1,0-W-acetyl-1-auraminy1-2,1,5-W-acetyl-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1-a-and-nyf-1
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Missing (in isoform 3). (FRIGWESP 001787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event-Alternative splicing; Named isoforms-3;
Comment-Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     normania (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- SIMILARITY: BELONGS TO THE GLYCOSTLTRANSFERASE FAMILY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMENAL, CATALYTIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes (ST6GalMAc III and IV): Characterization of their Spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG-VSP_001788.
7CF4101B8FDA369A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal-anchor; Golgi stack; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
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IsoId=09R2B6-2; Sequence=VSP_001788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            me=3; Synonyms=Short;
IsoId=09R2B6-3; Sequence=VSP_001787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                 MEDLINE=20198252; PubMed=10731711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40773 MW:
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EMBL: Y15780; CAB43515.1; -.
EMBL: Y15779; CAB43507.1; -.
EMBL: Y15779; CAB43508.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: X15779; CRB43508.1; -
EMBL: AJ007310; CAA07446.1; -
EMBL: Y19057; CAE93948.1; -
                                                                                                                                                                                                                  SEQUENCE OF 299-360 PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-1; Synonyms=Long 2;
IsoId-09R286-1; Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 CACTATGGATACATAAAAGAGAGAGAGAGAGAGAGATTTAGGAACTAGAACTATAACCTTTGT 405
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Kurosawa N., Liu H., Pircher H., Tsuji S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and functional expression of two members of mouse
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(NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc-alpha-2,6-sialyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
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787827010 (861. 41, 120000000

28-87827010 (861. 41, 1200 second outlete)

78-87827010 (861. 41, 1200 second outlete)

Alpha Wackeyl neuraminy-1,3-bets-galactosgi-1,3-80-
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                                                                                                                                                        US-09-714-936-218 (1-1294) x SI7C_MOUSE (1-305)
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SPLICING, AND DEVELOPMENTAL STAGE.
STRAIN-ICR, TISSUE-BIAIN;
         88.48
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117D M
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		TTATTIGGATCTGCGGGAATGTGGGGTGGAGAGGTCCTGCCGGTGGTACCAGGTCT 	TGCCCCAGGACTGCCCCTGACCCAGGCGCCCCCGCTGCTCGGTGGCAG	AGGGCCGGCGAGCCCAGGCCTGCATCCTGAAGACAAAGTCTGTGATGCTGTGATGCTGAGCT 	TORYNGCAGGGTTCCTTTTCCTGCTGGTTCTGGTAAATGAAGTGAATTTCCAT :::	CATTCTCCT HistenProAlaAlaP	TGGATACATAAATGTGAAGACACAAAG -GlytytSetSetValproAspGlyL	ACTGGACTGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGG :::	TTGGCCAGAAGGTGGGAATGGAGATAGATGGAFCCTCCTGCATTTGGAGAATGAACAATG ::	ACCAAAGGTTATGAAGAAGATGTCGGCCGCRTGACCATGATTCGAGTTG9GT 	WPACCAGCGTOCTCTTTGCTAAAAACCCGGATWTWTTTTCAAGGAATACT 	TGAGGAAAGATGGCAATGGCATCGTT 	ncracagotigrararagocagotiguscustocartocoraratatrostiguscago 	arcccatatgattactctgatgagtttttagaaggaarctgggaaggacaggg ::: argmetmetalatyrcysaspGlallePheGlaaspGluThrGlyLysasnargar		
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ative hes:	_	GAG	CCAGG	AAGAG	CGTCT	AAGTO	TATG	GCCAT	TCCT(CGCA7	SerH	PATGAC 	PCCGA rProG	PAAGA -::		AA. 197364 te) tate) tosyl-
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ARORES	MOUSE	GTGGG ::: Leu-A	CTGCC hrGly	rgleu	TGCTG	AACCT.	TTCGA	GTGAC	AGATA	AAAGAT 	TARAA :::	CTTTC	TTGGT	SATGGA	TCTACAGACACTTTT	PRT; 9; 09Y quence notati
et	SITD	GGAAT	CAGGA	CATGG	TTTTCC 11 eu-Cys	TGGAC 	3GCCCC 	CT	SAAATG yalag	ATGARG	TTTTG	3666AC	AGACAC :: InLeuf	ACTGTC 	£ :	09ULB eated st sex st an
8.38-31 415.00 54.91% 38.18% 17.42%	294) x (CTTATTTGGATCTGCGGGAATGTGGGCTGGA	AGCCTGCCCCCAGGACTGCC 	GAGCG	AGCAGGGTTCCTTTCCTGCTGGTGTGC :	TGCTACTAAACTGCTTTGGACAAO 	ACRCATACAGGGGGCCCTTCGAACTCACTATGGAT :::	AGCCTTTGCAACTGGAC :: ysproleulleargGlu	GGTGG	AGGTT	TCCTC	ATTGEGTATTEGGGACCTTCCGGAAA :::	GRAAA : :	GAGCGCATGAGTTACTGTGATGGAGT ::: ::: ::: ukrgketMetalaTyrCysAspGlnIl	ATGCAAGGGGACTGCTGATTTCTACAGACACTTTT ::: li!	T 4 (TSTD_EMMA STRUMED): UPPLY: 310,3 Ab. STRUMED: OBSERVED; STRUMED:
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rity:	218	CTTM	AGCC-	AGGG(:: spSer	TCATA ::: lava]	TGCT	Argse	AGCC7 ::	TTGG(:: euGl)	CCCCCC	ATAC	CTAT:	ACAA !!	AGAA 1::	AT of	AN 29NWU 29NWU 2003 (003 (acety
No.: s: nt Similarity Local Similar / Match:	-936-	38	38	149	209	269	320	377	434	164	554	514	674	734	794	AN D_BUM FEB-2 FEB-2 FEB-2
e: ent Sim Local; y Match	9-714															SULT 4 7D_HUM 28.71 28-1 28-1 28-1
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This STRES-STORY metry is opergright. It is produced through a collaboration between the Sease institute of Bioinformatics and the Budgean solutionsmitten institution. There are no restrictions on its library and the statement of the statement of the statement is not removed. Bease by and for commercial entities religious a library agreement (see http://www.isb-shib.cl/announce/or send an easil to librarealist-shib.cl).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rightment or 12-10; profile with M.A.

WINDLING-02939371, pubmed-1036919;

Gilley, Trind M.I.

Frement's green order differences within regions of conserved syntemy between the Toya and Imman genemes; implications for chromosomal volution and the caning 100 Global genes; implications for chromosomal volution and the caning 100 Global genes; implications for chromosomal volution and the caning 100 Global genes; implications to Green and the Caning 100 Global genes; or characteristic for characteristic for suppressing of MEMO-ALPANIA, 3-GALFANICES; or CHARACTER OF SUPPORTING TO GLODOSOMIPHS (89) GROUP TO GLODOSOMIPHS (89)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signery Front N. A. Markens S., Yomanaki M., Tashiro B., Ora T., Marachee, K. Kamagai A., Itakura S., Yomanaki M., Tashiro B., Ora T., Saudi S., C., Odovoda M., Wilshi T., Signer S., Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, expression and gene organization of a human NewSko alpha 2-38al beta 1-961Nkm alpha 2,6-slalyltransferase; hST66alNhcIV"; Blochem J. 323:37-48(2000).
acetylgalactosaminide alpha-2,6-slalyltransferase (EC 2.4.99.7)
(Namo-alpha-2,3-Gal-bera-1,3-GallMo-alpha-2,6-sialyltransferase)
(STGGalMac IV) (Stalyltransferase 7D) (Stalyltransferase 3C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetylneuraminyl-2,3-beta-p-galactosyl-1,3-N-acetyl-D-
galactosaminyl-8 - CMP + alphr k-acetylneuraminyl-2,3-beta-D-
galactosaminyl-8 - Galpha-N-acetylneuraminyl-2,6)-N-acetyl-D-
                                                                                                                                                                   Catarrini, Wortebrata, Buteleostomi,
Catarrini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                         Harduin-Iepers A., Stokes D.C., Steelant W.F.A., Samyn-Petit B., Ricceyinski-Recchi M.A., Vallejo-Ruiz V., Sanetta J.P., Auge C., Edianno P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim K.-W., Kim K.-S., Do S.-I., Kim C.-W., Lee Y.-C.;
"Molecular cloning of Neukochigat, Scalletel, Scallako alpha2,6-
Stallyltansferase ODNs. from human feral liver.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PARHWAX: Glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILATITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-acetylgalactosaminide alpha2,6-sialyltransferase.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                MEDLINE=20517254; PubMed=11062056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ271734; CAC07404.1; -. EMBL; API27142; AAF00102.1; -. EMBL; AB035172; BAA87034.1; -. EMBL; AK000600; BAA91281.1; -.
                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, (
Mammalia, Eutheria, Primates, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alactosaminyl-R.
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                                                                                                                                                                                                                                                                                                SECUZINCE PROM N.A.
                                                                                                                                                                                                                                 NCBI TaxID=9606;
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-1- PATHWAY: Glycosylation.
                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                   SEQUENCE FROM N.A.
               SITE_HUMAN
                                                          (9) euleuGlnLeuThrArgMetTyrProGlyLeuGlnValTyrThrPheThrGluArgMetM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443 AGGIGGBANIGAGAIAGAICGAICCICCIGCAIIIIGGAGAAIGAGAAIGACCOCCACA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 lyLeuGlyAlaGluIleAspSerAlaGluCysValPheArdMetAsnGlnAlaProThrV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AAGGITATGAAGAAGATGICGGCGCAIGACCAIGATTGGAGTTGIGICCCAIACCAGGG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 alGlyPheGluAlaAspValGlyGlnArgSerThrLeuArgValValSerHisThrSerV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 ITCCICITITGCIAAAAAAACCCIGAITAITITICAAGGAAGCGAATACIACIRIIGIG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           523 ITATITGGGGACCTITCCGCAATAIGAGGAAGAIGGCAATGGCAICGITIACAACAIGI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 etValTrpGlyGlnGlyArgHisMetAspArgValLeuGlyGlyArgThrTyrArgThrL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 TGAAAAAGACAGTTGGTATCTATCCGAATGOCCAAATATAGGTGACCACAGAGAAGCGCA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 TGAGTTACTGTGATGGAGTTTTTAAGAAGGAAACTGGGAAGGACAGGGCGTGCAAGGC 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 AACTGGAC---TGTGACCTTTGTGCCATAGTGTCAAACTGAGGTCAGATGGTTGGCGAGA 442
                                                                                                                                                                                                                                                                                                                             230 IGCIGG-------IIGIGGICIIGIAAAIGAAITICCAAIIGCIACIAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ValproGlyproLeuHisPheSer -- GlyTyrSerSerValProAspGlyLysProLeuv 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 alkrgGluproCyskrgSerCysklavalValSerSerSerGlyGlnMetLeuGlySerG 89
                                                                                                                                                                                                                                                                                                                                                                                                                     129 ----GGCGGCCCCTTGGAACTCACTATGGATACATAAATGTGAAGACACAAGAGCCTTTGC
                                                                                                                                                                                                                                                                                                                                                  26 CysTrpAlaGlyLeuProLeuCysLeuAla
                                                                                                                                                                                                                                                                                                                                                                        278 ACTOCITYGGACAACCIGGTACAAAGTGGAIACCAITCTCCTACACAIACA-----
                                                                                                                                                                                                                                                                                                                                                                                              36 ThrCysLeuAsp------HisHisPheProThrGlySerArgProThr
                                                                                          CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                              (GLCNAC. . .) (POTENTIAL).
                                             InterPro: TR8001675; Glyco_trans_29.
InterPro: TR8001675; Glyco_transt_29; 1.
Transferaes: Glycosyltransferaes: Glycoprotein; Transmembranes: Signal anchor; Gold; Stack.
                                                                                                                        IUMENAL, CATALYTIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                -> L (IN REF. 4).
08A4CDC749A6D783 CRC64;
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                                                                                                                                              N-LINKED (GLCNAC. . .)
S -> I (IN REF. 1).
ST -> QA (IN REF. 2).
                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                       US-09-714-936-218 (1-1294) x SI7D HUMAN (1-302)
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34200 MW;
EMBL: Y17460; CAB44334.; -.
EMBL: Y17401; CAB44334.; -.
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MIN; 606378; -.
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58.578
40.95%
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                                                                               Signal-anchor;
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CONFLICT
CONFLICT
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This sticks grow early is opergight, it is prediced through a collibration between the Saiss institute of joinformatics and the BRE collection on the burgeons bluckformatic institute. These are no restrictions on its way non-profit institutions as loop as its content at 1100 or 180 Schmidter R. D., Colling F. S., Wagner L., Shannon C. M., Schuller G. D.,
Misching R. D., Colling F. S., Wagner L., Shannon C. M., Schuller G. D.,
Misching S., Saberger M., Sancker M., S "idilizability", Tambardan, t., Yostofa, M., Restaudes, S., Tallada, S., Ooo Y., Moutura, T., Hitzada, S., Marahawa, K., Takkiguni, S., Kashon, S., Linda, S., Coo, Y., Marahawa, K., Takkiguni, S., Kashon, S., Linda, S., Kashon, S., Landa, S., human and mouse cDMs sequences. ", proc. Netl. Acad. Sci. U. S.A. 99:18899-16803 (2002). --- FRURTION: Innolved in the bicomynchesis of samplicatide GDls from SMB. It exhibits in Appear activities with glycolipide than with glycoprofeins (59 similarity). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelecstomi; Mammalia; Eutheria; Primates; Cataryhini; Hominidae; Homo. NCBA_TREF=6606; mentro irration (1875) (1970-17448 29.

Ffram: PROFINITY (1970-17448 29.

Ffram: PROFINITY (1970-17448 29.) 1. -! - SUBCELLULAR LOCATION: Type II membrane protein. Golgi (By -i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 29 TISSUB-Eye; MEDLINE-22388257; PubMed-12477932; EMBL; AK056241; BAB71127.1; -. EMBL; BC001201; AAH01201.1; -.

Signal-anchor; Golgi stack,

erPheLeu---SerThrGlv7rpPhe 216

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This STRES FOUR cutry in copyright. It is produced though a collideration between the Surs institute of Bioinformation and the EMEL outsettion. The Burgeas in Collidoration institute. There are no restrictions on its use To more profits institutions also so that the Amel of the Ame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 ADAGGCGGCCCTTCGAACTCACTATGGATACATAATGTGAAGACACAAGAGCCTFTGC 385
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. SPATRANT SUCCESSIVATION TYPE II SEEDINGE POOTEIN. GOLGI.
1. TISSUE REALITORYTH HOW PERESSIVEN IN PORSENATA MAD TO A LESSER
1. TISSUE REALITORYTH LAND. THE PERESSIVEN IN SPATRANT MAD TO A LESSER
1. LUNEA THE CREATELUAR. NO EXPRESSIVEN IN SALIVARY GLAMO, INTESTINE,
1. LUNEA, THORST, BELLAND, PHING SINCHERA, SALIVARY SELINGER OF THE GLYCOSYTPRANSFERSE FALIX 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Wolecular cloning of brain specific GDialpha synthase (ST6GalNAc V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okajima T., Fukumoto S., Ito H., Kiso M., Hirabayashi Y., Urano T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing CAGO/glutamine repeats...

J. 810.1 Chem. 274:30557:30562(1999)

-1- FUNCTION: Involved in the Inspiritesis of gangliceide UDIa fr. GAGD. It exhibits higher activity with giycolipids than with
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N-LINKED (GLCNAC. . .) (POTENTIAL)
MISSING (IN STRAIN C57BL/64)
MISSING (IN STRAINS C57BL/64) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase: Glycosyltransferase; Glycoprotein; Transmembrane;
LUMENAL, CATALYTIC (POTENTIAL).
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128516E3815985E6 CRC64;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
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Conservative:
Mismatches:
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EMEL; AB030836; BAA85747.1; ...
MGD; MGI:1349471. Siath. T.
ATD; PGI:1349471. Siath. Siath. Stath. Siath. Siat
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUE-Brain;
MEDLINE-99452943; PubMed=10521438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GInilesspührhrGlucysvalileargMetAsnAspAlaProThrargGlyTyrGly 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 CAACCTGGTACAAAGTGGATACCATTCTCCTACACATACAGGCGGCCC----- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 ---CTTCGAACTCACTATGGATACATAAATGTGAAGACACAAGAGCCTTGCAACTGGAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 TGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGAAGGTGGGAAAT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 CysArgAspCysAlaLeuValThrSerSerGlyHisLeuLeuHisSerArgGlnGlySer 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 GAGATAGATUGGATCCTCCTGCATTTGGAGAATGAAGAATGCCCCCCACCAAAGGTTATGAA 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 GAAGATGTCGGCGCATGACCATGATTCGAGTTGTGTCCCATACCAGGGTTCTTTTGG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIAAAAAACCCIGAITATTITTTCAAGGAAGCGAAFACIACIBITTGIGITATTGGGGA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 LeuArgAsnArgHisAspLeuLeuAsnValSerGlnGlyThrValPheIlePheTrpGly 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634 CCTTTCGGCAATATGAGGAAAGATGGCAATGGCATCGTTACAACATGTTGAAAAAGACA 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 SerGlnValLeuProArgLeuLysAlaPheMetIleThrArgHisLysWetLeuGlnPhe 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 GlyProArgProLeuAspGlyTyrLeuGlyValAlaAspHisLysProLeuLysMetHis 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090731 (20866).
2 PERS-2003 (Real, L1, Created).
3 PERS-2003 (Real
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            694 GTTGGTATCTATCCGAATGCCCAAATATACGTGACAGAGAAGAGGGCATGAGTACTGT
                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                              N-LINKED (GICHAC. ) (POTENTIAL).
N-LINKED (GICHAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                       (POTENTIAL).
"TMENAL, CATALYTIC (POTENTIAL).
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       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 GAIGGAGIIIIIIAAGAAGGAAACIIGGGAAGGACAGG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                       LUMENAL, CATALY
POLY-GLN.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-714-936-218 (1-1294) x SI7E_HUMAN (1-336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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137
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38 3
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137 1
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Best Local Similarity:
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CARBOHYD
CARBOHYD
                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                      SECUENCE
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151 ArgAspArgValAsnValThrMetIleArgGlySerAspGlyProPheAsnSerScrGlu 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 HisaspalaValLeuargPheasnGlyalaProValLysGlyPheGluGluAspValGly 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 GATTATTTTTTCAAGGAAGCG-----AATACTACTATTTGTGTTATTTGGGGACCTTT- 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 GlnGlnPhereulvs&spAlaieuTvrAsoThrGlvileIeuileValTrpAspProAla 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COGCABTATGAGGAAAGATGGCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (0.18W-1997 (Ba. 35, Carte segment)

10.18W-1997 (Ba. 13, Last segment)

12.5FBR-2007 (Ba. 14, Last annotation update)

12.5FBR-2007 (Ba. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 TrpGlnHisTyrLeuProAspLysSerLeuAsnGluThrValGlyArgCes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 TOCTOTICIACATTTICARCANTGARCANTGARCANTCOCACCANAAGGTTATGARGAAGGTCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 COCATG ACCATGATTCGAGTTGTGTCCCATACCAGGGTTCCTCTTTTGCTAAAAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 GlnLvsThrThrIleArgLeuValAsnSer-----GlnLeuValThrValGluGlu
                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                      PIR; S41114; S41114.
Interpro; 19R01675; Glyco_trans_29.
Fran. PRO77; Glyco_transf_29; I.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                       (POTENTIAL).
LUMENAL, CATALITIC (POTENTIAL).
BY SIMILARITY.
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-714-936-218 (1-1294) x SIA1_CHICK (1-413)
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                           EMBL; X75558; CAA53235.1; -.
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163.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 AA;
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                     90 ysMetHisCysLysAspCysAlaLeuValThrSerSerGlyHisLeuLeuArgSerGlnG 110
                                                                                  TGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAATGAACAATGCCCCCCACCAAAG 505
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                                                                                                                                                                                                GITATGAAGAAGAIGTOGGOGGCAIGACOAIGAITGGAGTIGIGICCCAIACGAGOGTIC 565
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Enkaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;
Ardossaukia; Vwes; Neoquathae; Galliformes; Phasianidae; Phasianinae;
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTES, BRAIN AND LIVER
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AND TO A LESSER EXTENT IN LUNG AND HEART.
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MEDLINE-94139712; PubMed-8307003;
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72.703-703 (Bel. 14, Last sequence update)
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SURPACE CARGOLORAPE DEFENDANTS GENERATED BY THIS BRIVNE.
-I: SIMILARIY: BELONGS TO THE GLYCOCYLTRANSFERASE PARLIT 29.
-I- DATABASE: NAME-PROM; NOTE-PROM 2.23-31 (2001).
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cochem. Biophys. Res. Commun. 164:225-232(1989).
H. PUNCTION: REMSERS STALIC ACLD FROM THE DOWOR OF SUBSTRAITE CMF-
- PUNCTION: REMSERS STALIC
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stath 2,6-stalytransferase; ', cathagain, 20,0,116:423-435(1992).
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Mammala; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Smeland E.B., Munderud S.,
"The B cell antigen CD75 is a cell surface sialytransferase.";
J. Exp. Med. 172:641-643(1990).
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SEQUENCE-0002581, PUMACA920225;
Mance P., Edu R.M., Man J.T.T.;
'Isolation and characterization of a partial cDNA for a human
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PATHWAY: Glycosylation.
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532 ACCATGATTCGAGTTGTGTCC----
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sialyltransferase CDNA.";
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TOPICATION. THANKSHEES STALLED AND FROM THE DORNO OF SHEETHARD CHO-
CASTALLY AND THE ALCOHOLOGY CONTINUES ALCOHOLOGY. SHEETHARD STALL AND THE SHEETHARD SHEETHARD THE SHEETHARD SHEETHARD THE SHEETHARD THE SHEETHARD THE SHEETHARD SHEETHARD THE SHEETHARD SHEETHARD THE SHEETHARD SHEETH
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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-1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 29.
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LUMENAL, CATALYTIC (POTENTIAL).
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(Alpha 2.6-ST) (Sialyltransferase 1) (ST6Gal I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94363344; pubmed-8081843;
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                                                                                                 ons musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                       SECURICE FROM N.A
                                                                                                                                                                                                                              NCBI TaxID-10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A MEAN DAY, LIKINGTON, DAY, MODELINGSHOW, R.P., KELB S.,
BELLINGSHOW, B.D., Modelindshow, D.D.
PERLINGSHOW, D.D., Modelindshow, D.D.
PERLINGSHOW, D.D.
PERLI
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                                                                                                                                                                                                                                                                            Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: CWP-N-acetylneuraminate + beta-D-galactosyl-

1,4-N-acetyl-D-glucosaminy1-giyoptoten - CWP + alibin N-

acetylneuraminy1-2,3-beta-D-galactosyl-1,4-N-acetyl-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES TESTED. HIGH EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALACTOSIDE ALPHA-2, 3-SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATHWAY: GİYCGGİLELGE
SUDCELLULAR LOCATON: TYDE II MEMBRANE PROTEIN. MEMBRANE-BOUND
FORM IT TRANS CISTERNAR OF GÖLĞI. SOLUBLE FORM IN BOOY FUCIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001675; Glyco_trans_29.
PERm; PP0077; Glyco_trans_29; 1.
TYRNSE_GRASS; Glycosyltransferass; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUMENAL, CATALITIC (POTENTIAL).
CLEAVAGE (FOUND IN SOME CHAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOUND IN BEALN, LIVER, KIDNEY, COLON, HEART AND LUNG.
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U1-FEE-1994 (Rel. 28, Last sequence update)
28-FEE-2003 (Rel. 41, Last ammoration update)
28-FEE-2003 (Rel. 41, Last ammoration update)
SABAYITEMSFERSE (EC. 24, 29, 6) (W-necyllastosmainide
SABAYITEMSFERSE (EC. 24, 29, 6) (W-necyllastosmainide
SABAYITEMSFERSE) (Gal beta-1, 3(4) GLONG alpha-2,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (P
16BAD1458963024C CRC64;
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                                                                                                                                                                       Stalyltransferase) (STSN) (Stalyltransferase 6)
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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                                                                                                                                                                                                                                                        Sattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                      WCBI_TaxID-10116;
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      white states offer earty is copyright. It is produced through a collaboration between the Suiss institute of Highlformston and the Digit outstands to bincopyring and mattriate where we no restrictions on its wast by non-poorts mattriate where we no restrictions on its wast by non-poorts institutions as longs as an operated in the nor wasternities requires a license agreement (see http://www.israth.cl/uncommon/or send no main! to licensesis-sho.sho.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 CyshlaValValSerSerAlaGlySerLeuLysSerSerGlnLeuGlyArqGluIleAsp 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 CGATCCTCCTGCATTTGGAGAATGAACAATGCCCCCACAAAGGTTATGAAGAAGTTGTC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 AspHisAspAlaValLeuArgPheAsnGlyAlaProThrAlaAsnPheGlnGlnAspVal 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 GGCCGCATGACCATGATTCGAGTTGTGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAAC 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 GlyThrLysThrThrIleArgLeuMetAsnSerGln------LeuValThrThr 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               583 CCTGATTATTTTTCAAGGAAGCG-----AATACTACTATTGTGTGTTTTGGGGACCT 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 SerValTyrHisSerAspileProLysTrpTyrGlnAsn----ProAspTyrAsn--- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            567 ATCGITTACAACAIGITGAAAAAGACAGITGGIATCIAICCGAAIGCCCAAAIAIGGIG 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
      WWW="http://www.ncbi.nlm.nlh.gov/prow/guide/343713755_g.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOMENAL, CATALYTIC (POTENTIAL).
BY SIMILARATY.
N-LINED (GLCNAC, ...) (POTENTIAL).
N-LINED (GLCNAC, ...) (POTENTIAL).
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BMBL, XGSSS, CAA35246.1; -
BMBL; RA7362; CAA44654.1; -
BMBL; A17362; CAA01327.1; -
PIR; A41734; A41734
Genew; RONC.10660; SIMI1.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Frem: PR00777; Glyco_trans_209.
Transerase; Glycosyltransekrase; Glycoprotein; Transmembrans;
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CATALYTIC (SOLUBLE FORM).
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                                                                                                                                                                                                                                                                                                                                                                    Biol, Chem. 267:2512-2518(1992).
                                                                                                                                                                                                                     TISSUE-Kidney, and Liver;
NRDLINE-92129335; PubMed-1733948;
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                                                                                              kidney transcripts.",
Glycobiology 1:25-31(1990).
                                                                                                                                                                                                                                                                                                                                            2,6-stalvitransferase gene,
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                          283 TITGGACAACCIGGTACAAAGIGGATACCATTCTCTACACATACAGGGGGGCCCCTTGGA 342
                                                                                                                                                                                                                     101 PheserLysProAlaProMetPheLeuAspasserPheArgLysTrpAlaArglleArg 120
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2.787200 (26.11). Care apparature update)
2.78720 (26.11). Care 
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Frimary structure of bearglactoside alpha 5.6-sfallyltensferase. 
Conversion of membrane-bound engine to soluble forms by cleavage of
     6.4
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STRAIN-Sprague-Dawley, TISSUE-Kidney, and Liver;
MEDLINE-92369623; PubMed-1983783;
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Indels:
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J. Biol. Chem. 262:17735-17743(1987).
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MEDLINE-88087067; Pubmed=3121604;
     5,818
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LA-GEORGY, THE OFF ACCESSATION OF THE ACCESSATION Wang X., O'Hanlon T.P., Young R.F., Lau J.T.Y.; Rat beka-galactocolde alpha 2.6-Salyltransferase genomic organization: alternate promoters direct the synthesis of liver and Wen D.X., Svensson B.C., Paulson J.C.;
"Tissue-specific alternative splicing of the beta-galactoside alpha of evel with the second specific and spec NEDIJNE-21246764, Pubbec-1178687;

Vonsarved cystaines R., Petalson J.C., O'Consarved cystaines In the stalylmosferase stalylmotifs form an vonsarved cystaines in the stalylmosferase stalylmotifs form an acceptable for the stalylmosferase stalylmotifs form an acceptable for the property of the stalylmosferase stalylmotifs form an acceptable for the stalylmosferase stalylmosferase and stalylmosferase stalylmosferase and stalylmosferase stalylm O'Hanlon T.P., Iau K.M., Wang X., Iau J.T.Y.)
"itsue-specific expression of beta qualactoside alpha-2,6sialyliranistarae. Transcript Reteropementy predicts a divergent Turson February 23, Sequence-VSF_001783; TISSUS SPECIFICITY: SYRONGLY EXPRESSED IN LIVER, SPLEEN, LUN KINNER AND SHEMAXILLARY GLAND AND WERALI IN HEART AND BEALN. PROTECLYTIC PROCESSING. -1- SIMILARITY: BELONGS TO THE GLYCOSYLFRANSFERASE FAMILY 29 -:- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY Event=Alternative splicing; Named isoforms=3; IsoId-P13721-2; Sequence-VSP_001782; IsoId*P13721-1; Sequence=Displayed; STRAIN-Sprague-Dawley, TISSUE-Kidney, MEDLINE-90008905, PubMed-2793863; Biol. Chem. 264:17389-17394(1989).

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This STRES FORT actry is expected. It is produced through a collaboration between the Suss institute of Bioliformatics and the BME outstation. The European and anoinformatic institute. There are no restrictions on its modified and pointormatic institute. There are no restrictions on the modified and point another and any as its content of a modified and another activities a license agreement (see http://www.isbrib.ch/amnonney or send an meant to I thomsee App.
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                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CATALYZES THE PORMATION OF THE NEURC-ALPHA-2, 3-GAL-BETA-
                                                                                                                                                                                                                                                                                                                                                                               1.4-GECRC-, NEURC-ALPHR-2,3-GAL-BERA-1,3-GLCNNC-OR NEURC-ALPHRA
2,3-GAL-BERA-1,3-GALINC-SEQUENCES FOXIN IN FERMINAL CARBORYBART
GROUPS OF GINCOPERINS AND GLYCOLFEIDS. THE HIGHEST ACTUTIT IS
TOWARD GAL-BERA-1,3-GLORICA AND THE LOFFER TOWARD GAL-BERA-1,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: CMP-N-acetylneuraminate + beta-D-galactosyl-
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      Chordata; Craniata; Vertebrata; Buteleostomi;
Rodentia: Sciurognathi; Muridae; Musinae; Mus
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- DEVELOPRENTAL STAGE. BURELORBENTAL REGULATION OMLY OCCURS IN

- LIVER, HERRY, KIDNEY AND SPLEEN.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4-N-acetyl-D-glucosaminyl-glycoprotein = CMP + alpha-N-acetylneuraminyl-2,3-beta-D-galactosyl-1,4-N-acetyl-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 29.
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LUMENAL, CATALYTIC (POTENTIAL).
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159 3
79 170
374 AA;
            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 ACMANGIGGAIACCAIICTCCIACACAIACAGGGGGGCCCTTCGAACTCACTAIGGAIAC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ThrGluTrp-----GluGlyTyrLeuProLysGluAsnPheArgThrLysValGly--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 ATRANTICIONAGRICANCANGAGOCTTTGCAACTGGACTGTGACCTTTGTGCCCATAGTGTA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGAATGAACAATGCCCCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCCATGACCATG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 LeuArgPheAsnGlyAlaProThrAspAsnPheGlnGlnAspValGlySerLysThrThr 225
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                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
MIHTNLKKKPSLFILVFLEAVICVWKKGSDYZALTLQAKE
                                                                                                                                                                                                                                                                                                                                                                               ATHTNLKKRFSLFILVFLLFAVICVWKKGSDYBALTLQAKE
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YLPKENFRTKVGPWQRCAVVSSAGSLKNSQLGREIDNHDAV
                                                                                                                              POMPKSOEKVAMGSASOVVPSNSKODPK BDITPILSYHRVTA
                                                                                                                                                            CVEROPSEOVEDSTESKINPRIEKIWRNYLAMMKYKVSY
GROGGVEFSVEALBCHIRDHYNVSMIRATDRPPRITTEMSS
                                                                                                                                                                                                                        ILPKENFRIKVGPWQRCAVVSSAGSIKNSQLGREIDNHDAV
                                                                                                                                                                                                                                                      LRPNGAPTDNFOQDVGSKTTIRLMNSQ -> MRYLLPWYGL
PHSYSOCVCHWTPASGISBNEPILISLILLYJGK (1)
                                                                                                                                                                                                                                                                                                                                                                                                             COMPREDEXVAMESASOVVESNSRODPKEDIPILSYHRVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVRPOPSPOVWDKDSTYSKLNPRIALKIWRNYL/NMNKYRVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRENGAPIDNPOQDVGSKITIRLANSO -> MRILIFWYGE
PHS (in isoform RKB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 SeralaGlySerLeuLysAsnSerGlnLeuGlyArgGluIleAspAsnHisAspAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598 AAGGAAGCGAATACTACT ----ATTTGTGTTTATTTGGGGACCT 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LyshspSerLeuTyrThrGluGlyIleLeuIleValTrpAspPro 256
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      (GLCNAC. . .).
(GLCNAC. . .).
(GLCNAC. . .) (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (in isoform RKB).
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Mismatches:
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16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 FTIG-VSP 001782
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Matches:
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N-LINKED (
N-LINKED (
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45.198
28.158
5.818
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      158
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Query Match:
DB:
      158
285
1
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      CARROHYD
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qq	161 ilevalGlyAsnGlyGlyValLeuAlaAsnLysSerl@uGlySerArgileAspAspTyr 180	use by non-profit institutions as lor
οy	AACAATGOCCOCAOCA	modified and this scattement is not removed, entities requires a license agreement (See Ma
B	181 AspileValileArgLeuAsnSerAlaProValLySGlyPheGluArgAspValGlySer 200	
ő	529 ATGACCARGATTCGAGTTGTGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAACCCTGAT 588	
g	201 LysThrThrBeuArgIleThrTyrProGluGlyAlaMetGlnArgProGlu 217	
ď	589 TATETTECAAGGAAGCGAALACTACTATTTGTGTTATTTGGGGGCCTTTCCGCAAT 645	DR GO; GO: 6008118; F:N-acetyllactosaminide alpha-2; DR interPro; IPR001675; Glyco_trans_29.
셤	118 GlnTyrGluArgAspSerLeuPheValLeuAlaGlyPheLysTrpGlnAspPheLysTrp 237	DR Pfam; PF00777; Glyco_transf_29; 1. KW Transferase; Glycosyltransferase; Glycoprotein;
δō	646 ATGAGGAAAGATGGCAATGGCATCGTTTACAACATGTTGAAAAGACAGTTGGTAFCTAT 705	Signal-anchor; Golgi stack. DOMAIN 1 8
g	238 Leufys 239	TRANSMEM 9 28
20	706 CCGAATGCCCAAATATACCTGACCACAGAGAACCGCATGAGTTACTGTGATGGAGTTTT 765	DOMAIN
g.	240TyrileValTyriysGluargValSerAlaSerAspGlyPheTrp 254	CARBOHYD 8U 80 N
QY	766 AAG 768	SMUCKINGE
g	255 Lys 255	ent Scores: No.: 9.36e-05
RES	RESULT 13	137.50
SIA6	STAC HUMAN STANDARD; PRT; 375 AA.	Local Similarity: 21.55% by Match: 5.77%
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10	01-0CT-1996 (Rel. 34, East sequence update)	US-09-714-936-218 (1-1294) x SIA6_HUMAN (1-375)
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100	stalltransferace (Gal betal.) (Archertransferace) 3 claittransferace (Gal betal.) 3(4) Glorac appa-2,3 claittransferace (Gal betal.) 3(4)	Db 102 PheSerEysProAlaProMetPheLeuAspAspSerPhe
85	SIATS.	Qy 343 ACTCACTATGGATACATAAATGTGAAGACGAAGAGCCT
888	Homo Sapiens (Human). Bukaryot, Metzeo, Chondata, Craniata; Vertebrata; Enteleostoni;	Db 122 GluPheValProProPheGlyileLysGlyGlnAspAsnl
385	Adminatra; Editablia; Primates; Catarrinin; Hominidae; Homo.	Oy 385CAM
Z 22 '	SEQUENCE FROM N.A.	Db 142 ValThrLysGluTyrArgLeuThrProAlaLeuAspSer
EX E	TISSUE-Flacenta; MEDLINE-93326146; PubMed-8333853;	OY 409 ATMOTOTCARACTCAGATGGTTGGCCAGAGGTG
RA	Kitagawa H., Paulson J.C.; "Cloning and expression of human Gal beta 1,3(4)GlcMac alpha 2,3-	Db 162 IleValGlyAsnGlyGlyValLeuAlaAsnLySSerLeu
R. R.	skalyltransferase."; Biochem. Biophys. Res. Commun. 194:375-382(1993).	Ov 469 TOTGGATTTGGAGAAAGGTAAAGGTT
88		
88	2,3-GAL-BETA-1,3-GALMAC- SEQUENCES FOUND IN TERMINAL CARBOHYDRATE GROUPS OF GINCOPROPERS AND GINCOLIDING THE HIGHEST ACTIVITY TO	
88	TOWARD GAL-BETA-1, 3-GECNAC AND THE LOWEST TOWARD GAL-BETA-1, 3-GALNAC HAY STATIABLEY.	
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888	acetylacurantnyl-2, 3-command 947 Cpt.com corr appla no acetylacurantnyl-2, 3-beta-D-galactosyl-1,4-N-acetyl-D-	ZY COS PARTITIONNOCHANGERINGTANTINGTOLINIT :::::::::::::::::::::::::::::::::::
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38	-I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY	706 CCGAATGCCCAAAT
38	PROTECTIC PROCESSING1- SIMILARITY: BELONGS TO THE GLYCOSYLFRANSFERASE FAMILY 29.	Db 241TyrileValTyrLysGluArgVal
9		Qy 766 AAG 768

duced through a collaboration as and the RMB1 outstation - are no restrictions on its its content is in no way lasse only and for commercial pps.//www.isb-sh.ch/announce.

Page 12

29 375 160 314 80 80 171 171 275 33 42171 MM2	MAIN, 606494; MAIN, 606494; GO; GO; 60069118; F; N°*-acety GO; GO; 60069118; F; N°*-acety Ffam; PR00777; G1yco_tran Ffam; PR00777; G1yco_tran Ffam; PR00777; G1yco_tran Ffam; PR00777; G1yco_tran Ffam; PR00777; G1yco	COMPANY NEWALTOBOOD SIGNO. (C) GOOGOBALL: F.N. *COCHOOLIBLE F.N.	(0) (0) (0) (0) (0) (0) (0) (0) (0) (0)	umacine
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δλ	343	343 ACTCACTATGGATACATAAATGTGAAGACACAGAGGCCTTTG384	384
g _Q	122	122 GlupheValProProPheGlyileLysGlyGlnAspAsnLeurleLysAlaileLeuSer 141	141
oy	385	385CAACTGGACTGTGACCTTTGTGCC 408	408
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142 ValThrLysGluTyrArgL@uThrProAlaL@uAspSerL@uArgCysArgArgCysIl@	409 ATMOTOTICARACTICAGGTCAGATGGTTGGCCAGAAGGTGGGGAAATGAGATAGAT	11eValGlyAsnGlyGlyValLeuAlaAsnLysSerLeuGlySerArgileAspAspTyr
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οy	529 A	GTCCCATACCAGCGTTCCTCTTT	888
qq	202 E	202 LysThrThrLeuArgileThrTyrProGluGlyAlaMetGlnArgFroGlu 218	218

255	241TyrileValTyriySGluArgValSerAlaSerAspGlyPheTrp 255	241	qq
765	706 CCGNATGCCCNAATHANGGGGACCACAGAAAGGGCATGAGTTACTGTGATGGATTTTT 765	706	97
240	239 LeuLys	239	qq
705	646 ATGAGGAAAGATGGCAATGGCATTACAACATGTTGAAAAAGACAGTTGGTATCTAT 705	646	QV
238	LeuPheValLeuAlaGlyPheLys	215	q
645	589 INTITITICANGGAAGGGAAINCIACTACIAITICIGIINIITGGGGACCITICGGGAAT 645	586	0.7
218	202 LysThrThrLeuArgileThrTyrPrcGluGlyAlaMetGlnArgProGlu 218	202	e e

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373 CAAGAGCCTTGCDA-----CTGGACTGCGACTTTGTGGCCATAGTGTGAAAC 420
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee; Mus
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                                                                                             Conservative:
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MEDLINE-94193584; PubMed-8144500;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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TISSUP-BENTYOLIC DYAIN;
TISSUP-SPAN W. BARBERCO, T., IRONE M., TSUJ1 S.;
MACHEGULAT CLORING And expression of chick Gal beta 1,3GalNNc alpha
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SUBCELDUAR LOCATON: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND
PORM IN TRANS CISTERANE OF GOLGI. SOLUBLE POPRE IN BODY FLUDS.
DEVELOPMENTAL STAGE: EXPRESSED IN BARLE EMBRYGNIC STAGES.
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Prem: PP0077; Glyco_trans_29.
Transferase: Glycosyltcansaferase; Glycoprotein: Transmembrane:
Transferase: Glycosyltcansaferase; Glycoprotein: Transmembrane:
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SIMILARITY: BELONGS TO THE GLYCOSTLTRANSFERASE FAMILY 29
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) N-LINKED (GLCNAC. .) (POTENTIAL). N-LINKED (GLCNAC. .) (POTENTIAL). 2801028F34A03E4D CRC64; MADD: M. ALGEDIO, SERVICE A. M. ALGEDIO, SERV (POTENTIAL). LUMBNAL, CATALITIC (POTENTIAL). BY SIMILARITY EMBL; X76989; CAA54294.1; -. 211 350 TRANSMEM DISULPID DOMATA

Conservative: Mismatches: Indels: Length: Matches: 000141 135.50 51.11% 37.78% 698 Similarity: Score: Percent Similarity: Alignment Scores: Pred. No.: Best Local S: Query Match:

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CARBOHYD

US-09-714-936-218 (1-1294) x SI4B_MOUSE (1-350)

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Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments) 5214.310 Million cell updates/sec 1 ocggaatttoogggtogacg......tttottotooctttttttg 1294 US-09-714-936-218 BLOSUM62 2383 Perfect score: Scoring table: Sequence: Title:

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Total number of hits satisfying chosen parameters: 328717 segs, 42310858 residues Searched:

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ALIGNMENTS

RESULT 1

APPLICATION TOWNS WHITE PRANCE, J. B.
APPLICANT: DWARF WHITE PRANCE, J. B.
APPLICANT: DWARF WHITE PRANCE CAN INTERCOME AND APPLICANT STRONG THE APPLICANT ST Sequence 75, Application US/09599360B Patent No. 6548633 GENERAL INFORMATION: JS-09-599-360B-75

NUMBER OF SEQ ID NOS: 123 SOFTWARE: Patent.pm SEQ ID NO 75 ORGANISM: Homo Sapiens NAME/KEY: SIGNAL LOCATION: -18..-1 US-09-599-360B-75 LENGTH: 302 TYPE: PRT FEATURE:

Length: Matches: Conservative: Mismatches: Indels: 382.00 58.574 40.954 16.038 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: ... 02

US-09-599-360B-75 (1-302)	TOCHG TO TRAINED TO TRAINED TO THE TOCK TOCK TOCK TOCK TOCK TO THE TOCK TOCK TOCK TOCK TOCK TOCK TOCK TOCK	278 ACTOCTHIGGACAACCTGGTACAAAGTGGACAACCCCCCTACACATAGA328	29GEGGGCCCTTTGGARCTACTATGGARACATAANGTGAAGACCTTTGG 385	886 AACYGGAC——TGTGACCTTTGTGCCATAGTGCTGAAGTCAGGTGGTGGCCAGA 442 [1]	14.13 AGSTGGGRAATGGARATGGTCGTCGTCATTGGAGAATGAACAATGCCCCACCA 502	003 AAGGTATGAAGAAGAYGTGGGCGGCAGAAGAACAYGAATGAGTGGTGCAATACAAGG 562 	563 TTOCTCTTTTOCTAAAAADCCTGATTATTTTTOAAGGAAACGAATACTACTATTGG 622	TTMTTGGGGACTTTCCGCAATATGAGGAAAGATGGCATGGTTTACAACATGT 682	9883 TORRARAGEMENTOGRAFFENCORATEOCORATECTRACTION TO THE THE THE THE THE THE THE THE THE THE	143 TONCTTACTGSTGATGSACTTTTTAGANGGANACTGGGAAGGGGGGCAGGGGGCATGCAAGGG 802 ::: ::: ::: ::	SCOROGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGOGO	PhyslyTrpPhe 216	5/09334601	iri.	SIALYLTRANSPERASES	7: US/09/334.601 -06-17
US-09-714-936-218 (1-1294) x US-09-599-360B-75 (1-302)	Oy 230 TGCTGG Db 26 CysTrpAlaGlyLeuP	Oy 278 ACTGCTTTGGACAACC Db 36 ThrCysLeuAsp	Qy 329GGGGGCCCCTTCG Db 50 ValProGlyProLeuB	Qy 386 AACTGGACTGTGA ::: Db 69 alargGluproCysar	OY 443 AGGTGGAAATGAGAI 	OY 503 AAGGTTATGAAGAAAA ::: 109 alGlyPheGluAlaAs	OY 553 TTCTCTTTTGCTAAAAA 	Qy 623 TTATITOGGGACCTTT ::::	QY 683 TGAAAAAGACAGTTGG	Oy 743 TGAGTTACTGTGATGG 	803	Db 209 erPheLeuSerThrGlyTrpPhe	RESULT 2 US-09-334-601-13 Sequence 13, Application US/09334601 Patent No. 6280989	GENERAL INFORMATION: APPLICANT: Kapitonov, Dmitri	AFFICAMIT IN MODEL STALTERANSFERASES TITLE OF INVENTION: NOVEL STALTERANSFERASES FILE REFERENCE: VCUIP-6	CURRENT APPLICATION NUMBER: US/09/334.601 CURRENT FILING DATE: 1999-06-17 MUMBER OF SEC 17 NOC. 06

Wed Sep 17 16:37:25 2003

TITILO DATE, advant 19, 1596 ATTORNEY, AGRET TREPREATURE, ALT. REGISTRYALTON NUMBERS, 31, 567 FREEDOMONICATION REPORMATION: TREEDOMONICATION REPORMATION: TREEDOMONICATION REPORMATION: TREEDOMONICATION REPORMATION: TREEDOMONICATION REPORMATION: TREEDOMONICATION REPORMATION: SURVEY, 202, 721, 2520 SURVEYER, 202, 731, 2520 SURVEYER, 202, 731, 2530	TREATER 1978 Main oadds TREATER 1978 MAINES oadd TREATER 1978 MAINES oadd TREATER 1978 MAINES OADD TREATER 1978 MAINES OADD TREATER 1978 MAINES OADD	1.93e-07	Percent Similarity: 42.488 Conservative: Best Local Similarity: 28.338 Mismatches: Query Natch: 6.158 Indels: DB: Gaps:	-09-714-936-	Oy 352 GGARGORARATGTGARGCGARGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	Qy 412 GrOrcharctchosrcorhischeosragosan ::::: Db 157 ValserseralaglyserleuLysasnSerslineuGlya	Oy 472 TGCATFTGGAATGAAAAAATGGCGCGCAAAGTTATG Dy 11	Cy 532 ACCATGATTCGACTTCTGTCC	Qy 553	Qy 565 CCTCTTTGGTBABABACCCTGATTATTGTTGABGBA [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	RESULT 5 US-08-446-777-4 ; Sequence 4, Application US/U8446777 ; Patent No. 5641568	GENERAL HYROPATION. APPLICANT: Berger, Eric G. APPLICANT: Wetzele, Manfred APPLICANT: Wetzele, Manfred	NVENTION: Proteins NVENTION: activity SEQUENCES: 8 SNOTE ADDRESS:	ADDRESSE: CIRA-GEIGY COMPORATION STREET: 520 White Plains Road CITY: Tarrycom. STREE: WYVON STREE: 10591-9005	
TELERY. TREATENANT TELESCA. TROOMACTON POOR SEQ ID NO. 8: SEQUENCE CHARACTERISTICS. TREATE: 176 action catcle of the catcle of t	Alignment Scores: 199e/77 Innegth: 376 Scores: 166.50 Marches: 32 Percent Sunitarity; 62.48 Conservative: 16 Percent Sunitarity; 83.374 Minnectnes: 36 Described. Sunitarity; 83.374 Minnectnes: 36 Described. Sunitarity: 36.374 Minnectnes: 36 Descr	-09-714-936-218 (1-1294) x US-08-666-3678-8 (1-376)	552 GARYCARAANGSTAAGAAGAGCCTTGCAACTGGAACTGGAACTGGAACTGGACCCTTGGTGCCCTTA 	0y 412 OTSCAAACTOSTABATOSTTGGCCRAAAAGGGAAACGGAACCTCC 711 (Qy 472 IGCATTGGAGAAGAATGGOCGCGACGAAGGTTATGAAGAAGATGTCGGCGCATG 531 D 1177 ALAVALLACATGATGATATGATATATGAAGAAGATGTCGCATATGA 531 D 1177 ALAVALLACATGATATATGATGATATATGATATATGATATATGATATATATGATATATATGATATATATATATGATATATATGAT	Oy 532 ACKTOATCOANGTOTOTOC 552 Db 197 Thirliansdawinalanserolndawilthringlunskropheledninskr 216		Oy 568 CCECTITECERAAAAACCTCGATATYTTCAACGAA, 603 Db 237 PCOLATYTYTCTAACAA, 11	RESULT 4 US-09-143-438-8	Sequence 8, hepitantion US/09134389 Sequence 8, hepitantion US/09134389 September 8, hepitantion US/09134389 September 8, hepitantion US/0913488 September 8, hepitantion US/0913488 September 9, hepitantion US/0	CING THE SAM	STREET, 1313 K Street, M.W., #800 CITY, Washington STATE, D.C., COUNTE, D.C.,	2 % E	OPERATION SYSTEM, MS-TOS (RESPYRADE) POSTERIES NS-TOS (APACCATOR) MINISTER NS-TOS-TOS FILING DAME: AMURE 28, 1598	CLASSIFICATION DOES: PRIOR PREPLICATION NUMBER: 08/666,367

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                                                                                                          IGAAGAAGATGTCGGCGCATG 531
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                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OFERATING SYSTEM: PC-DCS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DAYN:
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APPLICATION NUMBER: PCT/EP93/03194
APLICATION NUMBER: PCT/EP93/03194
PRIOR APPLICATION DATA:
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27 NOV 92
ADDRESSEE: CIBA-GRIGY Corporation
STREET: 520 White Plains Road
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; Patent No. 5641668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08,
FILING DATE: May 26, 1995
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MEDIUM TYPE: Floppy disk
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US-08-446-777-6
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APPLICANT: Netcale, Martind APPLICANT: Netcale, Martind APPLICANT: Netcale, Martind APPLICANT: Netcale, Martind APPLICANT: Netcale State of HARPHICANT: Netcale Marting OF HARPHICANT: Netcale Marting OF HARPHICANT STATE OF HARPHICANT STATE OF HARPHICANT STATE OF HARPHICANT STATE OF HARPHICANT STATE OF NETCAL STATE OF HARPHICANT STATE OF STATE OF HARPHICANT STATE OF STATE OF HARPHICANT STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF
                                       SOFTWARE: Patentin Release #1.0, Version #1.25 (RPO) CUBRENT APPLICATION DATA:
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Matches:
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 4-19361/A/BE
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CLASSIFICATION 435
APPLICATION NUMBER: PCI/EP93/03194
PILING DATE: 15 NOV 93
PRIOR APPLICATION DATA:
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FILING DATE: 27 NOV 92
ATTORNEY/8GENT INFORMATION:
                                                                                                                       APPLICATION NUMBER: US/08/446,777
FILING DATE: May 26, 1995
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5641668
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US-08-446-777-4
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Best Local Similarity:
Query Match:
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667 ATCGITTACAACAICTICAAAAAGACAGIIGGIAICTAICCGAAIGCCCAAAIAIACGIG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 TGTGACCTTTGTGCGATAGTGTGAAACTCAGGTCAGATGGTTGGCCAGAAGGTGGGAAAT 453
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Matches:
Conservative:
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Mismatches:
Indels:
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Matches:
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APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLLRANSFERASES
                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL SIALVIFRANSPERASES
FILE REFERENCE: VCUIP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILE REFERENCE: VOUTP-6
CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DREE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PREEMLIN VOR: 2.0
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
                                                                                          72-01
7 Sequence 20, Application US/09334601
7 Patent No. 6280989
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Patent No. 6280989
                                                                                                                                                                          APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
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SEQ ID NO 20
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US-09-334-601-21
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               APPIICANT: Berger, Riic G
APPIICANT: Watzele, Menired
APPIICANT: Transo, Svetoslav X.
TITILE OF UNEWEITON: Proteins having slycosyltransferase
FITHE OF UNEWEITON: activity
                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25 (EPO)
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Mismatches:
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RESISTRATION NAMESH: 36_134
RESPRENENCIOCCER NAMESH: 4-19361/A/BE
TELECOMMUNICATION INFORMATION:
FELEDRACH (908) 277-5306
INFORMATION PON SO) IN NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/EP93/03194 FILLW DAFE: 15 NOV 93 PRIOR APPLICATION DAYS: APPLICATION DAYS: APPLICATION NUMBER: EPO 92810924.8 FILING DAFE: 27 NOV 92 ATTORNEY/ARRY INFORMATION:
                                                                                                                                                   E: CIBA-GEIGY Corporation
520 White Plains Road
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, v
REMERRA PADILOZATON DAMA.
APPLICATION WOMER: US/08/446,777
FILING DATE: May 26, 1995
CLASSITICATION: 435
PRIOR APPLICATION DATA.
                                                                                                                                                                                                                                                                                           CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            Floppy disk
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LENGTH: 767 amino acids
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49.17%
29.17%
5.96%
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US-08-446-777-8
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MEDIUM TYPE: Floppy of
                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                             NUMBER OF SECUENCES:
                                                                                                                                                                                                 CITY.
STATE: NY
"TP: 10591-9005
"TP: 10591-9005
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RIKERAL INFORMATION:
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Dougry SetColi: 5-944 Tradels: 7	07 514 GARDANISTICATORING CANAGATICATORING CONTEXTORING 773	### ### ### ### ### ### ### ### ### ##	99 SerLysLeuGlnSerCysAspLeuPhe

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43 LeuargPheAsnGlyalaProThrAspasnPheClnGlnAspValGlySerLySThrThr 162
      418 AACTCAGGTCAGATGGTFGGCCAGAAGGTGGGAAATGAGATAGATGGATCGCTCCTGCATT 477
                                                                                                                                    123 SerAlaGlySerLeuLysAsnSerGlnLeuGlyArqGluIleAspAsnHisAspAlaVal 142
                                                                                                                                                                                                478 TOGAGAATGAACAATGCCCCCCACCAAGGTTATGAAGAAGATGTCGGCCGCATGACCATG 537
                                                                                                                                                                                                                                                                                                                        538 ATTOGAGIIGIGIOCCATACCAGCGIICCTCTTICCTAAAAAOCCIGATTAITITIC 597
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COMMUTER: IMA PC Compatible
OPERATION SYSTEM: PC PCDSA/95 DOS
OPERATES: PERCHITIN Relace File, Version #1.25
OPERATE PERCHITIN Relace File, Version #1.25
PELEN DEPERATION Relace File, Version #1.25
PELEN DEPERATION 1995
FILEN DEPERATION 131, 1995
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Mismatches:
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2029 Century Park East, Suite 3800
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Matches:
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Livingston, Brian Duane
Gillespie, William
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Patent No. 5858751
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FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Burlingame, Alma L.
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TELECOMMUNICATION INFORMATION:
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TELERAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 10:
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US-08-446-875-10
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PRIOR APPLICATION DATA:
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GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICARY: Medilingsky, Katalin
ITTLE OF INVENTIVA: Compositions and Methods for the
ITTLE OF INVENTIVA: Identification and Synthesis of Stalyltransferases
574 CTRABA------BACCCTGATTATTTTTCAGGAAGCGAAT 609
                                                57 AlaLysGluIleTyrAsnProAlaPhePheCysaspGluValAgn 71
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47
57
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CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
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1: 2029 Century Park East, 38th Floor
CA Angeles
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04-AUG-1993
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FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    Seguence 18, Application US/081023855
Patent No. 5962294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (310)788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,421
                                                                                                                                                                                                                                                                                    Paulson, James C.
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US-08-102-385G-18
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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Query March: 2,774 Todals: 45	69 469 TOTRO-FROM PROPER PROCESSOR AND PROCE	69 589 TATTITTCAAGAAGCAATACTATTGTOTTATT 1000SACCTITCOCQAA 645 Db 219 GLINTYGTURGEGEFER TARREST AND THE ALLY TETPOLASSACCTITCOCCAA 645 Cy 646 ANTAGGAAAANODCAATOGCATOTTTATAACATOTTATAAAAAGACTTGTATATT 705	239 239 504/29 240 240 240 240 240 240 240 240 240 240 241 2	DD 256 111 18 2017 14 356 5.0 18 20 2018 16 356 5.0 18 20 2018 20 5.0 18 20 20 20 5.0 18 20 20 20 5.0 18 20 20 20 5.0 18 20 20 20 5.0 18 20 20 5.0 18 20 20 5.0 18 20 20 5.0 18 20 20 5.0 18 20 5.0 1		TITIE OF IMPARTION INCHESTICATION TO SHADS TO SHADS THE SHAD THE S	CONTROL THE PROPERTY TO TOWN. VENUTRE INTO THE PROPERTY CONTROL THE PRO

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                                   82 MetGinProLeuLeuThrAlaGinAsnAlaLeuLeuGluAspAspThrTyrArgTrpTrp 101
                                                                          337 CTTCGAACTCACTATGGATACATAAATGTGAAGACAAAGAGCCTTTGCAACTGGAC--- 393
                                                                                                                                                                                    116 ThrileLysGluLeuPheArgValValProGlyAsnValAspProMetLeuGluLysArg 135
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                                                                                                                                             APPLICANT: BALLINGERS - Line 1.
TITLE OF INVENTION: Composition and Methods for the TITLE OF INVENTION: Composition and Synthesis of Stalyltransferases TITLE OF INVENTION: Identification and Synthesis of Stalyltransferases
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Matches:
Conservative:
Mismatches:
Indels:
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2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, ocuRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
                                                                                           Livingston, Brian Duane
Gillespie, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/102,385
FILING DATE: ANGUSE 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
Sequence 16, Application US/U8446875
Patent No. 5858751
                                                    APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
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TRLEARA: (310) 777-1297
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
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135.50
35.478
22.648
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MEDIUM TYPE: Floppy d
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PRIOR APPLICATION DATA:
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US-08-446-875-16
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CORRESPONDENCE ADDRESS:
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                                      INFORMATION:
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USA
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                 Patent No.
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PUTTERNATION

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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nucleic - protein search, using frame_plus_n2p model ĕ

(without alignments) 6789.824 Million cell updates/sec September 12, 2003, 15:04:59 ; Search time 60.5 Seconds Run on:

1 coggaatttocgggtcgacg.....tttcttcttcttcttttttg 1294 US-09-714-936-218 2383 Perfect score: Sequence:

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2215726 Total number of hits satisfying chosen parameters: 1107863 segs, 158726573 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summeries Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greeter than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT

AAB21617 standard; Protein; 363 AA (first entry) 16-JUL-2002 AAE21617;

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ABP64885 standard; Protein; 221 AA
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                                                                                                                                                                                                                                                                                                                                                                 I, Soppet DR, Olsen HS;
Choi GH, Fiscella M:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seventeen nucleic acid molecules encoding human secreted proteins, useful for treating and preventing cancer, immuse disorders (e.g. Addisor) disease, and allergies), and cardiovascular disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
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Shi Y, Cho
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Duan DR,
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                         SerSerCys11eTrpArgMetAsnAsnAlaProThrLysGlyTyrGluGluAspValGly 120
                                                                             526 OGCARGACCATGATFCGAGTFGFGCCCATACCAGGGTTCCFCFTTTGCTAAAAAACCT 585
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threspectic protein X and Maman albumin (Ha, also Known as human serum 
albumin, HSA), The proteins are useful for treating a disease on re-
                                                                                                                                                                                                                   161 MetArgiysaspGlyasnGly1leValTyrAsnMetLeuLysiysThrValGlyIleTyr
New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Albumin fusion protein, therapeutic protein X; human albumin; HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunomodulator; anti-HIV; antidiabetic; haemostatic; noottopic; neuroprofective; antiparkinsonian; antimicrobial; neuroleptic; setopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human serum albumin, HSA, cancer: reproductive disorder:
disestive disorder; immune disorder; endorine disorder,
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cytostatic; antiinfertility; antiinflammatory; antiuloer;
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25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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                         Zhao OA:
                                                                                                                                                                               New isolated polynucleotide, useful in research, diagnostic or 
farapeutc methods, e.g. preventing or treating disorders involving 
aberrant protein expression or biological activity
                         Asundi V, Zhang J,
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                         Liu C, Zhou P,
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Human albumin fusion protein #1841
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25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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Pi Rosen CA, Konstoulis GA, Baker FF, Birse CE, Sopper DR. Olsen BS; Pi Moore PA, West P. Enner R. Dean DR, Shi Y. Choi GH, Fiscella M; Pi M 13; A 1202-11564/3. DR WT-1 2002-11564/3. DR WENGER Models of Companies C amount of the host protein in a smaple or by determining the presence of control of the mutations in the more genes. Specific uses are described for each of the tensor of the tissues in which they are most highly expressed, and include sewiciping products for the disposals or treatment of connect, and include sewiciping products for the disposals or treatment of connect control of the connect control of the control of the connect control of the control of the connect control of the control of t	CC conduction disponders, and infections. The proteins can also be used to add conduction disponders, and infections. The proteins can also be used to add common healing and epithelial soil proliferation. To present skin skin skin conduction to the conduction of t	Alignment Scores: 166e-112 Length: 305 Score: 1100.00 Metches: 277 Score: 1100.00 Metches: 277 Score: 278 Scor	166 Argacotroancotranagaaaancrotraantootrotroancotroanacotrocotrocotrocotrocotrocotrocotrocotr	Of the Control of the	4.1 at Journe of yhritystrapidae robbserry yhritystrapidae robbsery hit. 346 cacemonan canamano caanacan canaman canaman ill. 6.1 METY OLYTHIANAN LIYAHOO 160 ILL. CANAMAN CAN	Op 0.000 MARTIN CONTRACTION OF CONTRACTION OF CONTRACTION CONTRACT	
286 GARAACCYGORAAANTGARACTCCCTCCACACAAACGGGGGGCCCACACACACACACAC	Section Sect	Or 766 Maskagemakenskoningson 769 Db 201 LysEysturhacijujakeparg 208 RESULTS ANSLEYS STANDARD FORCERS 308 ANSLEYS STANDARD FORCERS 308 AA.	Ruman, 2002 (first entry) Ruman game 1 encoded secreted protein MESPR39, SEQ ID NO:50. Ruman, secreted protein, prolifestive disorder aconsor; numour, AIDS; forein, abnormality developmental, haseastopistic disorder. AIDS; forming system, endformsoular; and oppositive forming and oppositive forming and oppositive forming and oppositive forming and oppositive forming and oppositive forming and oppositive, neutrological, autoimmune diseases	Parkinson's disease; Schinophrenia pectials; segsis, a becombined in pertinson's disease; schinophrenia pectials; segsis, a becombined green farapy.	200	Protein 31335 Alabal McUne_secreted_protein R020022554-A1. 21.9AR-2002.	17-7A#-2001, 2001WG-0501385. 12-5EP-2000, 2000US-211959P. (SIDAA-) RUBAN GENOME SCI INC.

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285 286 GGACAACCTGGTACAAAGTGGATACCATTCTCCTACACATACAGGGGGGGCCCTTCGAACT 345 465 81 AlaileValSerAsnSerGlyGlnMetValGlyGlnLysValGlyAsnGluileAspArg 100 585 121 ArgMetThrMettleArgValValSerHisThrSerValProLeuLeuLysAsnPro 140 646 ATGAGGAAGGTGGCAATGGCATCGTTACAACATGTTGAAAAAGACAGTTGGTATT 705 166 ATGGCCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTT 225 21 PheleuleuValValargieuValarsGluValarsPheProleuleuleursCysPhe 40 09 346 CACTATGGATACATAAATGTGAAGACACAAAGAGCCTTTGCAACTGGACTGTGACCTTTGT 405 466 TCCTCCTGCATTTGGAGAATGAACAATGCCCCCCACCAAAGGTTATGAAGAAGATGTCGGC 525 GATTAITITICAAGGAAGCGAAIACIACIATITGTGTATITGGGGACCTTCCGCAAT 645 141 AspTyrPhePheLysGluAlaAsnThrThrIleTyrVall1eTrpGlyProPheAraAsn 160 1 METALACYSTIGLOULYSARGLYSSERVALIDEALBYALSERPHEILEALBALAPHELOU 20 61 HisTyrGlyTyrIleAsnValLysThrGlnGluProLeuGlnLeuAspCysAspLeuCys 80 41 GlyGlnProGlyThrLysTrpIleProPheSerTyrThrTyrArgArgProLeuArgThr 226 TICCTGCTGGTTGTGCGTCTTGTAAATGAAGTGAATTTCCCAFTGCTACTAAACTGCTTT 526 CGCATGACCATGATTGGAGTTGTGCCCATACGAGGGTTCCTCTTTTGCTAAAAAACCCT 901 586 à a ă a 8 g õ 셤 ö

Birse CE, Soppet DR, Olsen HS; Shi Y, Choi GH, Fiscella M;

Komatsoulis GA, Baker KP, Wei P, Ebner R, Duan DR,

Moore PA, Ni J; Rosen CA,

2002-315684/35. N-PSDB; AAD34123.

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(HUMA-) HUMAN GENOME SCI INC.

12-SEP-2000; 2000US-231969P.

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Claim 11; Page 450-451; 483pp; English,

161 MetArgLysAspGlyAsnGlyIleValTyrAsnMetLeuLysLysThrValGlyIleTyr 180

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presence of tumours, such as prostate and breast tumours, in mammals and 
to sereen if or modulators of the compounds -
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                    Gurney AL;
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                    Godowski PJ,
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Smith V, Watanabe CK, Rood WI, Zhang Z;
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                                                PRO Polymeptide: mammal; tumour; cancer; human; cattle; horse; sheep; dog; ter; plsy goot; rabbit; tumour necrosis factor alpha; Wive-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; cell addition of the decinal; lung; breast; prostate; rectum; cervix; luver; genetic disorder.
CCGAATGCCCAAATATACGTGACCACAGAGAAGCGCATGAGTTACTGTGTGAGGTTTTT 765
                                                                                                                                                                            201 LysLysGluThrGlyLysAspArg 208
                                                                                                                                          766 AAGAAGGAAACTGGGAAGGACAGG 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide sequence #268.
                                                                                                                                                                                                                                                                                                                                                         AAU29291 standard; Protein; 210 AB
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02-4AR - 2000) 2000WC USD5941.

03-4AR - 2000) 2000WS-187202P

06-4AR - 2000) 2000WS-18596RP

14-4AR - 2000) 2000WS-18932RP

14-4AR - 2000) 2000WS-18932RP

14-4AR - 2000) 2000WS-18932RP
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2000WO-US13705.
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2000US-193032P.
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Treatment and firs nucleic enid molecule are useful for the diagnosis, 
textement and prevention of discorders associated with increased or 
decreased expression of DME. Examples of such discorders include.
ATGAGGAAAGATGGCATGGCATCGTTTACAACATGTTGAAAAAGACAGTTGGTATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drug metabolizing enzymes and encoding solymucleotides, useful for diagnosing, treeting and/or preventing autoimmue, inflammatory, cell proliferative, developmental, endocrine, eye, metabolic, and
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Hillman JL, Yue H, Atalmeal Y, Yao MG, Gandhi AR;
Tang YF, Lal P, Bandman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human drug metabolising enzyme (DME-17) protein.
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/note= "Sialyltransferase"
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                                                                                                                                                                                                                                         66 AAGAAGGAAACTGGGAAGGAC 786
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAE05186 standard; Protein; 210
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28-JAN-2000, 2000US-0178574.
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Ring HZ, Hillman JT.
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ABU71379 standard; Protein; 210 AA

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		20-MAR-1998; 27-MAR-1998; 27-MAR-1998; 31-MAR-1998;							29-APR-1998; 29-APR-1998;			07-MAY-1998; 07-MAY-1998;				18-MAY-1998; 22-MAY-1998;		28-MAY-1998; 02-JUN-1998;			04-JUN-1998;			05-JUN-1998; 05-JUN-1998;	09-JUN-1998;	-					12-JUN-1998; 12-JUN-1998;			17-JUN-1998;
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		PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood; necrosis factor alpha release; chondrocyte cell; proliferation; nflation; tumour; gene therapy.																																
(first entry)	Human PRO7177 protein.	Human, PRO, secreted, transmembrane, cyltumour necrosis factor alpha release, cl differentiation, tumour, gene therapy.				2002US-0187600.	98WO-US19330.	-US25108.	-USI0733.	99WO-USI2252.	99WO-US2109U. 99WO-US28301.	99WO-US28551. 99WO-US31274.	2000Wo-US00219. 2000WO-US04341.	2000WO-US04342.	2000WO-US05004.	2000WO-US05841.	Z000WO-US08439.	2000WO-US13705.	2000WO-US14941. 2000WO-US15264.	-US20710.	-US30952.	2000WO-US34956.	2001WO-US17800.	2001WO-US21066.	2001WO-US21735. 2001WO-US27099.	97US-059263P. 97US-059266P.	97US-062250P.	97US-063120P.	97US-063540P.	970S-063544P.	97US-063584P.	97US-064103P.	97US-065311P. 97US-066120P.	97US-066466P. 97US-066772P.

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Smith V, Watanabe CK, Wood WI, Zhang Z;
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286 GGACAACCTGGTACAAAGTGGATACCATTCTCCTACACATACAGGCGGCCCCCTTCGAACT 345
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                                                                       41 GlyClnProGlyThrLysTrpIleProPheSerTyrThrTyrArgArgProLeuArgThr 60
                                                                                                                                  Human; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
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Page 18

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Y	346	CACTATGGATACATAAATGTGAAGACACAAAGAGCCTTTGCAACTGGACTGTGACCTTTGT 405	
۵	61	HisTyrGlyTyrileAsnValLysThrGlnGluProLeuGlnLeuAspCysAspLeuCys 80	
¥	406	GCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGAT	
۵	81	AlaileVaiSerAsnSerGlyGlnMetVaiGlyGlnLysVaiGlyAsnGluileAspArg 100	
ž.	466	TCTCCTCCTGCATTTGGAGAATGAAGAATGCCCCCACCAAAGGTTATGAAGAAGATGTCGGC 525	
۵	101	SerSerCys1leTrpArgMetAsnAsnAsnAlaProThrLysGlyTyrGluGluAspValGly 120	
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۵	161	MetargiysAspGlyAsnGly1leValTyrAsnMetLauLysLysThrValGly1leTyr 180	
'n	706	COGRATGCCCAAATATACGTGACCACAGAGAAGCGCATGAGTTACTGTGATGGAGTTTTT 765	
,Q	181	ProAsnalaGinileTyrValThrThrGluLySargMetSerTyrCysAsp6lyValPhe 200	
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101 SerSerCysIleTrpArgMetAsnAsnAshProThrLysGlyTyrGluGluAspValGly 120

645

586 GATTATTITTTCAAGGAAGCGAATACTACTATTTGTGTTATTTGSGGACCTTTCGGCAAT

161 MetarqlysAspGlyAsnGly1leValTyrAsnMetLeulysLysThrValGly1leTyr 180

706 COGNATOCCCARATATAOGTGACCACAGAGAGCGCATGAGTTACTGTGATGGAGTTTTT 181 ProAsnalaGlnileTyrValfhrThrGluLysArgMetSerTyrCysAspGlyValPhe

646 ATGAGGAAGGINGGCAAIGGCAICGITIACAACAIGITGAAAAAGACAGIIGGIAICTAI 705

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OWNO-1599 (TARBELLE, 12, Lest sequence update)
01-907-1599 (TARBELLE, 12, Lest sequence update)
ACT-2002 (TARBELLE, 12, Lest sequence update)
Alpha-W-overlydalactocomaine alpha-2,6-sialyltransferase
                                                                                                                                                                             35409 MW; 7EC434C948F8B599 CRC64;
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                                                                                                                                                        Hypothetical protein.
SEQUENCE 305 AA:
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Sujyama T., Title R., Outulf T., Salor C. H., Makahira H., Jiflall S.,
Yamana C., Jacon T., Kasai-Hio, Y., Saito K., Mishikawa T.,
Kimora K., Sansailta H., Watton K., Makamura Y., Saito K.,
Kikochi H., Anda K., Magasama H., Wirakawa K., Manahori K.,
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Mammalia; Ettheria; Primates; Catarrhini; Hominidae; Homo.
NCBE_TARIP=9606;
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01-057-2002 (TERMELE). 22 Created)
01-MAR-2003 (TERMELE). 22 Last sequence update)
01-MAR-2003 (TERMELE). 23 Last annotation update)
MONO SEptens (Human).
                                         Conservative:
Mismatches:
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                   PREMIATE/STRUCTS INSERDEMENTARY GLACK;
PRINTED 5194561; PRAME 51245681;
PRAME 51878 CHORN BEAR CHILD RESERVE GROUP Plane I & II Team;
"NAMALYSE Of the Inches treasering conservations based on functional annotation of the Translation of the Child Property Child Structure (Nobes.);
PREMIATE OF THE STRUCTURE OF TH
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01-0CT-7000 (TEMBLEL 15, Last sequence update)
01-0CT-2002 (TEMBLEL 12), Last annotation update (GalNoc alpha-2,6-sialyltransferase (Fragment).
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MEDLINGS-9929920/, Pubmed-10369878,
SZILBY J. Pried M.; "Extensive gene order differences within regions of conserved synteny
              Pugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Dalkaryota Menzaca: Grafuska: Crainides Verdebrits: Butelostcal;
Actinopterygii Noopterygii, Takaostel; Butelosstel; Necelaostel;
Acanthocorpha, Acanthopterygii, Parcooperpla; Tetraodoutiformes;
Tetradoutsides; Tetraodoutides; Zakfugu.
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Bakaryda. Metazos; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Euthenta; Rodentia; Soiurognathi; Muridae; Murinae; Mus.
MCBLTaxID=10090;
                                                                                                                                                                                                                                                                                                          between the Fugu and human genomes: implications for chromosomal
volution and the cloning of disease genes.";
Hum. Mol. Genet. 8:1313-1320(1999).
RSBL; Y17466; ChR44388.1: -.
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01-007-202 (FEBRITA-1.2) Last sequence update)
01-007-202 (FEBRITA-1.2) Last sequence update)
01-007-202 (FEBRITA-1.3) Last sequence update)
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                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoat;
Kommalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TAXID=10090;
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68 PheHisTyrGlySerLeuArgGlyArgThrArgArgProValAsnLeuLysLysTrpSer 87
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Mondata; Vertebrata; Buteleostomi; Padrayota; Muscula (Mouse).
Monmala; Butheria; Rodentia; Schurognathi; Muridae; Muskammala;
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01-ARR-2003 (TEMBLER, 23, Created)
01-ARR-2003 (TEMBLER, 23, Last sequence update)
01-ARR-2003 (TEMBLER, 23, Last annotation update)
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MEDLINE-22354683; PubMed-12466851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 AGABAGTOTOTOTOTIGOTGTGTGTGCTTCATAGCAGGGTTCCTTTTCCTGCTGGTTGTGCGT 243
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107 PheProAsnWetGluAlaTyrAlaValSerProAlaArgMetGlnGlnPheAspAspLeu 226
                                                            163 TITAAGAAGGAAACTGGGAAGGAAGGAAGGAGGCAAGGCGACTGCTGATTTCTACNGAC 822
                                                                                                                                                                                                                          246 TrpPheThrMetValileAlaValGluLeuCysAspHisValHisValTyrGlyMetVal 265
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Odoljam T., Chen H., Ito H., Kiso M., Tai T., Furukawa K., Urano T.,
Purukawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryote; Metacos; Chordata; Craniata; Vertebrata; Enteleostomi; Mommalla: Entheria; Rodentia; Sciurognathi; Muridae; Musae; Mus. NEEL, PartD-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-007-2000 (TPEREL-61. 15, Created)
01-007-2000 (TPEREL-61. 15, Last sequence update)
01-007-2002 (TPEREL-61. 22, Last annotation update)
0501 alpha/571a alpha/601b alpha synthase.
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TISSUE-stain, and Muscle;
Strauberg R.; Szbarderg R.; Szbarderg R.; Szbarted (GTT-2001) to the EMBL/GenBank/NDBJ databases
EMBL; Scoll6299; AMBLG290.1.; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 LeuhrgVallleGlnhrgAlaGlyLeuMetPheProAsnMetGluAlaTyrAlaValSer 218
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                                                                       154 CGGCGGAGCGCCATGGCCTGCATCCTGAAGAGTCTGTGATTGCTGTGAGCTTCATA 213
                                                                                                                                                                       314 GCAGCGTTCCTTTTCCTGCTGGTTGTGCGTCTTGTA-------AAT 252
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                                                                                                                       33 ArgardArgCluMetSerSerAsnLysGluGlnArgSerAlaValPheVal-----
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Riwaryota Motizoro (Obordia: Craniata; Vertebrata; Euteleostomi;
Riwaryota Motizoro (Obordia: Sciucognathi; Muridae; Murinse; Mus.
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WADDLMR-2234503; Burbked-1246881;
The FARNON COnsortium:
the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                       68 Gluyal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 CAAGAGCCTTTGCAACTGGAC------
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*Analysis of the mouse transcriptome based on functional annotation of 60,770 full-langth nobMas, "; states 420:655-731 (2002).
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Mommalia; Butherla; Perimates; Catarrhini; Hominides; Homo.
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PRT; 335 AA.	3, Created) 3, Last segu 3, Last anno	ata; Craniata; Vertebrata; Buteleostomi; tis; Sciurognathi; Muridae; Murinae; Mus.	SEXENCENTE FOR M.A. MENTARCHESTING, STATEMENT CHARGED AND ASSESSED 23 Langth: 535 MacDales: 535 MacDales: 56 Massaches: 5 Index: 2 Gaps: 2	x Q8CBX1 (1-335)	ACCOUNTED A ACTROCOMPACA OF CONTROL OF THE STATE OF THE S	ACAGGCGGCCCCTTCGAACTCACTATGGATACATAAATGTGAAGACACAAAAAGCCCTTTGC 385	IntenciuGlyTyrLeuGlyValAlaAspHisLysProLeuL 89	AACTGGACTOTGACCTTTGTGCCATAACTGCAGTTGAGCTCAGATGGTTGGCCAGAAGG 445	PROGRAMMENCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	4 4		CTCTTTTGCTABABAACCCTGATTATTTTTTTCAAGGAAGCGAATACTACTATTTTGTGTTA 625	InArglieLeuArgAspArgHisAspLeuLeuAsnValSerGlnGlyThrValPheIleP 169	TTTGGGGACCTTTCCGCAATATGAGGAAGGCAATGGCATCGTTTACAACATGG 685	19	AAAAQACAGTIGGIATCIATCCGAATGCCGAAATRACGIGACCACAGAGAAGCGCAYGA 745 	789	euGlnPheAspGluLeuPheLysGlnGluThrGLyLysAspArg 223		
PRELIMINARY;	rel. 23 rel. 23	Mus musculus (Mouse). Bukaryota, Metazoa, Chordat. Mammalia: Butheria; Rodenti. NCBI_TaxED=10090;	Signame FROM N.A. MEANING-CTALLAGEST, TESSUP-piencephalon MEDILAGESTS-GASS, PANAGE-1246651, P	es: 1.89e-22 314.50 rity: 88.52% ilarity: 38.07% 11arity: 13.20%	218 (1-1294)	ACTGCTTTGGACAACCTGGTACAAAGT ThrGlySerThrGlnLeuValGluSer	ACAGGGGGGGGGTTGGAA	ProAlaGlyProArgGli	AACTGGACTGTGACCTT	TGGGAAATGAGAZAGATG	INCLYSTORISILERSPO		CTCTTTGCTAAAAACC	lnArglleLeuArgAspi	TTRGGGACCTTTCCGC	heTrpGlyProSerSerf	AAAAGACAGTTGGTATCT	GTTACTGTGATGGAGTT	euGlnPheAspGluLeuf	
DBCBX1	AC 08CBX1; DT 01-MAR-2003 (TIEMBI DT 01-MAR-2003 (TIEMBI DT 01-MAR-2003 (TIEMBI DF 01-MAR-2003 (TIEMBI DF 01-MAR-2003 (TIEMBI	Mus musculus (Mo Bukaryota; Metaz Mammalia; Buther NCBL_TaxID=10090	SECTIONS SET SECTIONS STRAINS STRAINS THE PRIVE THE PRIVE THE PRIVE THE PRIVE THE PRIVE THE PRIVE THE PRIVE THE PRIVE SECTIONS SE	Alignment Scores: Pred. No.: Score: Percent Similarity: Destruct Similarity: Destruct Similarity: Destruct Similarity:	US-09-714-936-	278	326	70	386		109		266	149	10	0.0	186	9	209	RESULT 12

RESULT 11

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111 AsnLysThrThrPheArgValValAlaHisSerSerValPheArgValLeuArgLySPro 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AlaGluCysThrIleArgMetAsnAspAlaProThrSerGlyTyrSerAlaAspValGly 110
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Memmalia, Butherla; Primatas, Catarrhini, Hominidae, Homo.
Largarie-9606,
                                       SEQUENCE 295 AA; 33947 MW; DDE04DA7CF6CDAFA CRC64
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01-Mar-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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Wismatches:
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Homo sapiens (Human).
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Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Muriaes; Mus
MOBI_eratho=10090;
                                                                                                                                                                                                       Homo sapiens (Human).
Boro sapiens (Human).
Borkaryota; Hetazoa; Chordata; Cranista; Vertebrata; Buteleostomi;
Mammalia; Ruthorka; Primates; Catarrhin; Hominides; Homo.
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01-ARX-2000 (TPSBMILE.) IS, Last sequence update)
01-007-2000 (TPSBMILE.) IS, Last sequence update)
Noveryquateroseminide alpha2,6-skalyltransforase (Fragment).
STATF OR STGALMAN VI.
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01-0CT-2000 (TEMSELE). 15, Created)
01-0CT-2000 (TEMSELE, 11, Last sequence update)
01-0CT-2002 (TEMSELE, 12, Last amortation update)
005-60H13 (Similar to stalyitranferase) (Fragment).
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Matches:
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TISSUE-Liver;
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Best Local Similarity:
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181 AAGAGAAAGTCTGTGATTGCTGTGAGCTTC --- ATAGCAGCGTTCCTTTCCTGCTGGTT 237
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                                                                                                                                                                                                                                                                        Bikaryota; Metaron: Chordata; Craniata; Vertebrata; Euteleostomi;
Mommalia; Eutheria; Primates; Catarrhini; Bominidae; Homo.
WCBI_TAXID=9606;
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Berdain Appeter A.:
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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Pram. PF00777; Glyco_trans_29; 1.
Sp(008717; Glyco_trans_29; 1.
Sp(00881transferase, Transferase, S99 AA, 34,29, WW; P90AFP04008A0C5F CRC64;
                                                                                                                        Ol-MAY-2000 (TPREMILEA). 13, CREATE, 13, CREATE, OL-MAY-2000 (TPREMILEA). 13, Last sequence update) ol-OCT-2007 (TPREMILEA). 12, Last sequence update) K-acety_galactoramide Alpha2, 6-sial_pltransferase. SFGGARMO.
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Mismatches:
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Best Local Similarity:
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TISSUE=Liver;
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Pram: PR09777; Glyco_trans_29, 1.
Mypothetical protein.
SEQUENCE 299 Ax; 34261 MW; 10022760412224BBD CRC64;
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Matches:
Conservative:
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Query Match:
DB:
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Search completed: September 12, 2003, 16:36:28	Search completed: Sep Job time : 117.5 secs	Sear
208 LeuSerThrolyTrpPhe 213	208	q
808 CTGATTTCTACACACTTT 828	808	ζŽ
188 GlnPheAspAspLeuPheArgGlyGluThrGlyLysAspArgGluLysSerHisSerTrp 207	188	q
748 TACTGTGRIGGRGTTTTTRAGAAGGAAACTGGGAAGGACAGGGGGCATGCAAGGCGRCTG 807	748	Q.
168 argalaGlyLeuValPheProAsnMetGluAlaTyralaValSerProGlyArgMetArg 187	168	셤
688 AAGACAGTTGGTATTCCGAATGCCCAAATATACGTGACCACAGAGAGCGCATGAGT 747	688	δō
TrpGlyProProSerLy	149	g
628 TOGGGACCITICCGCAATAGAAGAAGAAGAAGCAATGGCAATGGCATTACAACATGTTGAAA 687	628	ď

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5.1.6 Compugen
version - 2003
GenCore (c) 1993
Copyright

OM nucleic - protein search, using frame_plus_n2p model

(without alignments) 6913.460 Million cell updates/sec September 12, 2003, 16:29:54; Search time 36 Seconds Run on:

2383 - - 2383 - Contraction of the contraction of t US-09-714-936-218 Perfect score: Sequence:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameters: 283308 seqs, 96158682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

***WORDET**(Erine**, JR; p. 1972-47).

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***PACTO

Database :

pir_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•					
Result No.	Score	Query	Query Match Length DB	DB	£ £	А	Description
-			1	İ	-		
-1	163	6.8	413	7	841114	9	Gal beta 1,4 Glc
c	142	6.9	406	2	A41734	ı,	beta-dalactoside
m	138.5	9.9	374	2	A45074	9	Gal beta 1,3(4)G
4	138.5	80.	403	c	A28451	ж	beta-qalactoside
s	137.5	9.0	375	c	JN0618		Gal beta 1,3(4)G
9	136	5.7	342	a	S55675	9	Gal-beta-1,3GalN
-	135.5		350	N	B54420		beta-qalactoside
90	135.5		350	ca	A54420	.4	beta-galactoside
6	134	5.6	340	C	I54229	4	betg-galactoside
20	131.5	5.5	350	C	JC5251		beta-galactoside
11	131	5.5	337	C	\$36824		oeta-qalactoside
13	126	5.3	380	ď	JC6321		CNP-Neuho-GM3 al
13	125.5	5.3	343	2	A45073	9	Gal beta 1,3GalN
77	124	5.5	380	2	856950		alpha-2,8-sialvt

alpha-2,8-sialytra

protein T23G18.14	hypothetical prote	gal-beta(1-3/1-4)G	alpha-2,3-sialyltr	Gal beta-1, 3GalNA	BCL6 homologous zi	alpha-N-acetylgala	GM3 alpha-2,8-sial	lactosylceramide a	alpha-N-acetylgala	alpha-N-acetylneur	alpha-N-acetylneur	N-glycan alpha 2,8	sialyltransferase	STX protein - huma	sialyltransferase	hypothetical prote	probable integral	inding pro	alpha-2,8-polysial	related to CYCS pr	serine proteinase		hypothetical prote		primase - ateline	gamma-crystallin 4	natural killer cel	alpha-N-acetylneur	polysialyltransfer	ubiquinol-cytochro
G86216	T49278	248715		A54871	JC7812	JC7248	JC4973	JE0364	A49880	JC5195	A54032	148686	139169	B54898	A4 6727	T00720	T36683	T30257	159403	T51016	534583	T14106	T27506	T47524	T42970	CYMSG4	PT0375	22	S52425	8
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123	120	118.5	118.5	116.5	113	112	111	110	110	108	106	103	101	100	100	97.5	95	92.5	92	92	92	91	89.5	88	88	87.5	87	87	00	86.5
15	16	17	13	13	20	21	22	23	54	52	36	27	28	50	30	33	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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ALIGNMENTS

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A.Cross.references: MMBL:X75558; NID:q452750; PIDN:ChA53235.1; PID:q452751 C;Superfamily: beta-galactoside alpha-2.6-sialyltransferase

Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	163.00				2
Alignment Scores: Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	

413 47 59 47 59

Gaps:

	- NI/-60-SD	936	US-09-714-936-218 (1-1294) x S41114 (1-413)	
,	δλ	343	343 ACTOACTATGGATACATAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGCCTT 402	102
-	QD	131	lahlaLysLe	150
•	6y	402		402
-	q	151	151 ArgAspArgValAsnValThrMetIleArgGlySerAspGlyProPheAsnSerSerGlu 170	170
_	λō	403	-TGT 405	405
	qq	171	171 TrpGlnHisTyrLeuProkspLysSerLeuAsnGluThrValGlyArgLeuGlyArgCys 190	190

465 GOCARATHOTOTOAACTVAGCTACACTGGCAGAAGGCGAGAATGGTGAAGGGAATGGTCAA 465	GATCGA 465	C;Reyords: glycoprotein; glycosyltransfernes; Golgi apparatus; transmenhrane protein P;10.28/Domain: transmenhrane stratus proteited «The F;145,75/Danials sites: carbohydrase (Ann) (covatan) stratus predicted	Golgi apparatus; transmembrane proteii i <pre><pre><pre><pre><pre></pre></pre></pre></pre></pre>
	GFCGGC 525	Alignment Scores: 0.000158 Length: Pred. Mo.: 142.00 Matches: Percent Similarity: 49.173 Conservative: Incer Loval Similarity: 49.173 Mismarchies	406 406 35 41179: 24 41
dy 526 CGCATGACCATGATTCGACTGCCCATACCAGGGTVCTCTTTTGCTAAAAAACCCT Db 11	AACCCT 585 Gludiu 247	2.96%	
dy 586 GATAVTTOTTCHAGGARGGCAATACTACTAPTTOTGCTATTGGGGAGCTTT- 639 DD 248 GINGIRPHGLEWIGRAFDALAUTYTAGHTN-CLYTIALAULIGVALTFASPPTOALA 267	CCTTT- 638	18-19-114-190-2012 1-1-2012 20	rgccagaaggroggaargaar 462 :::::
OY 639 COCCAMPTWORDARACTGGGANTG6	665 sGluAla 287		GCCCCCACCAAAGGTTATGAAGAAGATGTC 522
Og 666	57		RACCAGCGTTCCTCTTGCTAAAAAC 582 FGIn
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Cisperais Mono Saplans (mm) Cipterais 10-bg-1039 sequence serision 30-sep-1999 text_change 24-Sep-1999 Cisperais 10-bg-1039 sequence RA3443 (1903)25 SBIZE Cisperais 10-18 ci Zibol, Li Treemen, G-J. (Colley, K.J., Ernst, T.J.; Munro, J.M.; Teel Rast, B-J.S. (Cipterais Cipterais Sep-1999 .J.; Munzo, J.M.; Ted	637	TICCGCARTATGAGBAAGATGGCAATGGC 666	
J. (6H 1801. 116, 475-43), 193. J. Katesene number: A41734; Mat CDF6 differentiation antigens are unique A; Ratesene number: A41734; WAID:92112963; PRID:1730763 A; Recession: A41734;	que cell-surface cari	Oy 667 ATGUTTACANCHICTHGANANGCAGCHGTHACTARCCGAATGGGCAAATGGCCAAATGGCTG 726 Db 277PheficheStabenTytLysThrTytAcGUSsealtskroadGlnproPhefytLie 295	ANTICEATCCGAAGGCCCAARTARGGTG 726 sleufisproashGlipropheryrile 295
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Fishenmandroric, 7. Askies, M. C.; Desperchi, A.; Blomboff, B.K.; Smeland, E.B.; Funderud, J. Exp. Med. 172, 611-663, 1990 Aprille: The Be call antique Ordy is a ceal untrae sushyitzmerierase. Aprille: The Be call antique Ordy is a ceal untrae sushyitzmerierase. Aprille: The Second number; Jupple; MIDI-9623464; MMID-3273955	land, E.B.; Funderud,	A spekerackom mumberi AA5074; NUTD:93016017; PNID:1400416 A:Accessorio: AA5074 A:Sections profilementary A:Accessorios type; mRAN, protein	D:1400416
Almostania such type: mARM Almostania type: mARM Almostandes 1.75 (T. /24.71, T. /14.143, TP./145-406 <5TA.) Almostandes: GENEXASS; MID:929388; PIDM:CAA38344.1; PID:929389 Almostandes: GENEXASS; TIAT Daudid (PERKITA Type)	688	Airtoss-references: GB:AF774, GB:A994622, NID:9206930; PIDN:ABAN2146.1; FI A:Rocelamical Bource: Library Bouchone (NIB:RIR:116197, NIB:PI:116191) A:Rocelamical extracted from NIB: Bockbone (NIB:RIR:116197, NIB:PI:116191) A:Rocelamical extracted from NIB:ABANCAN (NIB:RIR:116197, NIB:PI:116191) A:Rocelamical extraction extracted from NIB:ABANCAN (NIB:RIR:116197) A:Rocelamical extraction for the complex of the	9206930; PIDN:AAA42146.1; PID:9206931 (WCBIN:116167, WCBIP:116191)
Rilance, p.: Liun, M.W., Lian, J.T., Lian, J.T., Bellense, Biochem, Biophys. Res. Commun. 164, 225-232, 1989 Affilts Tacklichon and Commun. 1984. 2016. 1989 Afficience number: 333444, MUDI-9002681; phDD:2602395 Afficience number: 333444, MUDI-9002681; phDD:2602395 Afficience number: 304044, MUDI-9002681; phd. 2016. 2	cDNA for a human stalyltransferase. 95	Alignment Socres: 0.00037 Length: Pred. Nav. 2000 131 131.00 Macches: perpending 131.00 Macches: perpending 131.00 Macches: perpending 131.00 Macches: perpending 131.00 Macches: perpending 131.00 Macches: perpending 131.00 March 131.00 Mar	374 : 39 BILVE: 34 hes: 63
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238	6y 296 ADANOSCIAROZATOCHAURACHADOZAGOSTICAROZAGOSTICAROZAGOSTICA 357 Db 150 Michitel		186	Qy 478 TGGARGARTGARCCACCACCAAGGTRATGAAGAAGATGCGGCGCCACATGACGATG 10	0y 538 ATPOGAGTEGROCOMEACHACHACHTTTTGGTAAAAACCTGATTATTTTTC 597	598	Db 242 IyakspSerLeuTyrThrGluGlyTleLeuTleValTrpAspPro 256	RESULT 5 JN0518	Gal bera 1,37(4)CtMc alpha-2,3-stalyltransferase (BC 2.4.99) - human C:Species: Homo septems (man) - the second (man) - the control of the	C.AccessAon Alvola R R.Kitogawa, H., Peulakon, J.C. Biochem. Biophys. Res. Commun. 194, 375-382, 1993	A:Title: CLORING and expression or numan Gallocal, 2(4) Gallock alpha#, 3 salayittense. A:Reference number: JW0518; WID:93326146; PMID:8333853. A:Reference number: JW0518; WID:93326146; PMID:8333853. A:Reference number: JW0518.	A. Residue v. 1957 math. A. Residues 1. 375 et 1122768; NID:1388014; PIDN:AAN35778 1, PID:1388015 A. CCCOSS-TREEgenes: GB:1427768; NID:1388014; PIDN:AAN35778 1, PID:1388015 C. COMMENT: This energy me cotalyzes the transfer of stalic ncid to the terminal positi.	C.Superfamily: alpha-2,3-stalyltransferase ST\$ C:Reywords: glycosyltransferase	Length: Matches:	t Similarity: 40.338 ocal Similarity: 21.558 Match: 5.778	Gaps: 18 (1-375)	dy 283 TTFGGACAROCTGGTACAAAGTGGATACCAATGCTCAAAGATACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	dy 343 MOTONCTANGGARANATOROAAGAOQOAGAGCETTG	Qy 385CAACTGGACTGTGGGCTTTGTGCC 408	Db 142 ValThrLysGluTyrArgLeuThrProAlaLeuAspSerLeuArgCysArgArgCysIle 161	Oy 409 ATAROTENANGORGHARATORIOCORAMAGANTARAMATATAROTC (68 IIIIII III III III III III III IIII III IIII
dy 343 ACTACKNORMORMANDTRANDGERARGOCHTG0	141 Valfhriysglufyrargieuthrproaleieua 409 atagrecaacteggeeggeeggeeggeeggeeggeeggeeggeeggeeg	693	Db 181 AspilevalileArgiaukSnSerAlaProValLySilyPhaciluiysAspValidiysar 200 S39 ArgaCcArgaVproAnGTGPOCCOKTACCAGGGTPCGTGTFTGGTBAAAAAAAAAA 588	201	OY 599 TRITITIONAGGORARIANTATIVICITIATI TGGGGACTITCCCCAAN 645 ::: :::::::::::::::::::::::::::::::::	OY 646 ATGAGGAAGATGGCAATGGCATTAGAAGATGTAGAAAAAGACAGTTGGTATGTAT	706 CCGAATGCCCDAATATATACGTCACCACAGAGAGCGCAGGAGTTACTGTGAGGAGTTTTT	240	0y 766 AAG 768	SULT 4	heta-qalactoside alpha-2,6-sialyltransferase (BC 2.4,99.1) - rat Nalterate pames CMP-Verghatranhiste-alpha-N-acetyl-galactosamide-alpha-2,6-sialy S.Species: Batris nervosi(nos Nervos set)	C.harte: 13-AMN-1599 sesquence_restsion 19-Nay-1989 *text_change 24-Sep-1999 C.hartession. 26461; A34465 R.Weinstein. 3-; Lee, E.G.; McEntee, K.; Lai, P.H.; Paulson, J.C.	J. Biol., Chem. 262, J.733-17743, 1987 A.Jītle: Primary structure of beta-qalactoside alpha-2,6-sialyitransferase. Conversion of A;8efecance number: A28451; BIOTE-88097067; PMID:3121604	A.Noceasion A28451 A.Noclecule type: mnA A.Residuce: 1.403 <wri></wri>	A.Cross-references: GB-AH3763, WID:GOAL254, PIDN:AAA41196 1, FID:g001355 A.Kross-references: GB-AH3763, WID:goAL254, PIDN:AAA41196 1, FID:g00135 B.O Handon, T.F.: Law. R.M.: Rang, X.; Law. J.T.E.	J. BADI, CHEM. 7444 IN399-17394, 1389 A.Title: Tissue-specific expression of beta-galactoside alpha-2.6-stalyltransferase. Tra A.Reference nucleor: A34465; MUID:90008905; PWID:2793863	A.Richasaluri Aridon A.Richaus: preliminary; not compared with conceptual translation A.Richaus: preliminary; not compared with conceptual translation A.Richasilus: USA 245, 352-292, COMA>	An operation bottom; bottom; bottom; bottom; bottom; constitution of C.Superfamily; bed-equicocoide alpha-2,6-stalyltransferase C.Naywords; glycosyltransferase; transmembrane protein	No.: 0.000328 Length:	larity:	5.81% Indels: 2 Gaps: 94) x A28451 (1-403)

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à	493 GCCCCACCAAAGGTTATGAAGATGTCGGCCGCATGACCATGATTCGAGTTGTCC 552	ð 5	439 CAGAAGGTGGGAAATGAGATGATCGATCTCTGCATTGGGAGAATGAAT
a	182 AlaProThrValGlyPheGluGlnAspValGlySerArgThrHis 197	3 8	COLOGE LYLOLYTHOG PURITHER SPORT THE SECTION OF THE
රු සි	553 CATACCAGGGTTCCTCTTTGCPAAAAAACCCGGATAYTTTTTCAAGGAAGGGAAGCGATACT 512 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	S 8	The Val Girphe Gladia As Para Color
6	ACTATTEGERAL TERROR 642	6. F	559 AGCGTCCTCTTTGCTAAAAACCCTGATTATTTTCAAGGAAGG
eg G	213 SerPhevalLeuvalProPhoLys 220	3 8	9
RESULT S36824 Deta-ga	11 Llactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - mouse	ē fi	asy Workstrathoodactriftcool 64. 200 AsnNetValleuValbroPhelys 207
C; Spec. C; Date:	C;Species: Mus musculus (house mouse) Scheit: 22-26m.1994 #sequence_revision l3-Mar-1997 *text_change 24-Sep-1999 C;Arceseion: 974824	RESULT 1 JC6321	RESULT 12 CONTRACTOR C
R;Lee, Bur. J. A;Title	Ribee, X.C.; Kurosawa, N.; Hamamoto, T.; Nakaoka, T.; Tsuji, S. Bur 7. Stochem. 256, 377-382, 1933 "Affitie: Molecular clonian and expression of Gall-beta-1,30alNic-alpha-2,3-sialyltransfer	N.Altern C.Specie	
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Copyright (c) 1993 - 2003 Compugen Ind. OM nucleic - protein search, using frame_plue_nbp model Run on: September 12, 2003, 16:3744; Seetch 189 Seconds Full cor: September 12, 2003, 16:3744; Seetch 199 Seconds Full cor: September 12, 2003, 16:3744; Seetch 199 Seconds Full cor: Seetch 12, 2003, 16:3744; Seetch 199 Seconds Full cor: Seetch 12, 2003, 16:3744; Seetch 199 Seconds Second 12, 10:394, 10	segg, 145912426 selgy, 145912426 selgy, 145912426 selfyfig chosen (200000000) mm Match 1006 mm Match	CARPERGO CARPERGO CARPERGO CARPERGO CARPERGO	Pred. No. is the number of results predicted by chance to have a some spracker than or equal to have a some spracker than or equal to have some of the result hamby prinched, and is derived by analysis of the noisk score distribution. \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$

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PRODE APPLICATION WINGSER: 60/A63541 FRICE APPLICATION WINGSER: 60/A63544 FRICE PILLING MARKE: 1987-90-26 FRICE PILLING DATE: 1987-91-26 FRICE PILLING DATE	Alignment Scores: 1,03e-101 Length: 210 Sreal-Mo.: 1035-101 Length: 206 Scores: Spillarity: 99-234 RemarkDRs: 1 Dest Local Stallarity: 99-234 RemarkDRs: 1 DB:: 25,924 Index 0	DS-09-714-296-738 (1-1244), NOS-10-194-497-736 (1-1210) OF 166 HOROCOPOLAMAGEMATICOMERATION TO THE PROPERTY TO THE THE PROPERTY OF THE THE PROPERTY OF THE THE THE THE THE THE THE THE THE THE	21 Philaidean (1972)	0y 346 COURTORORACEACARACTERADACACATERDAGETEROLOGICE ACCOUNT 4105 E1 LINITALY CASTALLANDER COURTOR COURTOR 4105 EQ COURTOR CASTALLANDER COURTOR CASTALLANDER COURTOR CASTALLANDER COURTOR CO	0 46 TOTOCOCCENTERCAGE AND COCCOCCESSOR ASSESSOR ASSESSOR ASSESSOR OF 25	07 586 GENERALTEROLOGOGIA PER ANGEL	706 COGRACOCOCORANTALOS COCACACACACACACACACACACACACACACACACACAC	REGION A C45-256 C55-256 C
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NUMBER OF SEQ ID NOS: 612
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Mismatches:
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201 LysLysGluThrGlyLysAsp 207
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Best Local Similarity:
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                                                                           Godowski, Paul J.
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US-10-184-642-536
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MetalaCysileLeuLysArgIysSerValileAlaValSerPheileAlaAlaPh6Leu 20
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Publication No. US20030166188al
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APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
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APPLICANT: Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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46 CACTATGGATACATARATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGT 405
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Publication No. US20030166106A1
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US-10-173-691-536
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CURRENT FILENE DATE: 1002-06-17 FILE APPLICATION REMOVED. See File Wrapper or Palm FILE APPLICATION FROM STATE MODERN OF SEE TO NOS: 612 FIRE REPRESENT FROM SEE TO NOS: 612 FIRE REPRESENT FROM SEE TO NOS: 612 FIRE REPRESENT FROM SEE TO NOS SEE TO NOS MANUEST FROM SEE TO NOS MANUEST FROM SEE TO NOS MANUEST FROM SEE TO NOS MANUEST FROM SEE TO NOS FIRE REPRESENT FROM SEE T	Alignment Socrete 1.03e-101 Length: 220 Socrete Socrete 1.03e-101 Machine 2.00 Socrete Socializative 2.00 So	08-09-714-936-928 (1-1394) x 08-10-171-694-536 (1-210) QY 156 (10-210) x 08-10-171-694-536 (1-210) QY 156 (10-210) x 08-10-171-694-536 (1-210) DE 10-10-171-171-171-171-171-171-171-171-17	286 41 346 51	0 0 0 0 0 0 0 0 0 0	SEG GETTATETT CHARACTURA CONTINUE CONTI	07 7/06 CONTROLLED TO THE CONT
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Sequence 536, Application US/10173699 Publication No. US/20030166109A1 GENERAL INPORMATION:

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TITLE OF INVENTION: SERENTED AND TRANSMEMERAND POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                           Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                           FILE REPERENCE: P3430R1C12
CURRENT APPLICATION NUMBER: US/10/173,698
CURRENT FILING DATE: 2002-06-17
APPLICANT: Goursey, Austin I. SPELICANT: Pen, James APPLICANT: Smith, Victoria APPLICANT: Watanabe, Colin K. APPLICANT: Wood, William I. APPLICANT: Zhong, Zemin APPLICANT: Zhong, Zemin
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US-10-173-698-536
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US-09-714-936-218 (1-1294) x US-10-173-698-536 (1-210)

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Dp	21	PheLeuLeuValValArgLeuValAsnGluValAsnPheProLeuLeuAsnCysPhe 40
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qq	41	GlyGlnProGlyThrLysTrplleProPheSerTyrThrTyrArgArgProLeuArgThr 50
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qq	61	HisTyrGlyTyrlleAsnVallysThrGlnGluProLeuGlnLeuAspCysAspLeuCys 80
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qq	81	AlaileValSerAsnSerGlyGlnMetValGlyGlnLysValGlyAsnGlulleAspArg 100
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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APPLICANT: Baker, Kevin P.
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US-10-173-699-536
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CURRENT FILLING NAME: 2002-06-18
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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Publication No. US20030166111A1
GENERAL INFORMATION:
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                                                 161 MetArgLysAspGlyAsnGlyIleValTyrAsnMetLeuLysEysThrValGlyIleTvr 180
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Gurney, Austin L.
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
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105-02-103-86 (08-1)
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                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Result No.

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Chen, Rui-hong
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ray, Yunging
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: AsundA, Vinod
APPLICANT: AsundA, Vinod
APPLICANT: Shang, Jie
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US-09-620-312D-401
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Wang, Zhiwei
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Best Local Similarity
                                                                                RESULT 3
JS-09-620-312D-401
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533 ACCTTTCCCCAATATGAGGAAAGATGCCAATGCCATCCTTTACAACATGTTGAAAAGAC 592
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Setches 234; Conservative 0; Mismatches 226; Indels 0
                                                                                                                                                                                                                                 753 TGATGGAGTTTTTAAGAAGGAAACTGGGAAGGACAGGGGGCA 794
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CHRENK PAPLICATION NOWER: 19,09/334,601.

CHRENK PETLING DARE: 1999-66-17

SOFFWARE: PETCHIN DAY: 2.0
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Sequence 12, Application US/09334601
Patent No. 6280989
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US-09-334-601-12
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
833 CTCTTCAAGCAGAGACTGGCAAAGACAAGG 852
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Patent No. 6569662
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144 GGCCTGGTGTTCCCCAACATGGAAGGTTATGCCGTCTCTCCCGGCCGCATGCGGCAATTT 803

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393 CTGTGACCTTTGTGCCATAGTGTCTAAACTCAGGTCAGATGGTTGGCCCAGAAGGTGGGAAA 452
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TITEL OF INVENTION: Compositions and Methods for the
TITEL OF INVENTION: Teletification and Synthesis of Stalyltransferases
VINDES OF SEQUENCES: 16
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Best Local Similarity 55.5%; Pred. No. 6.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product- "porcine Gal Beta 1,3
OTHER INFORMATION: GalMAc alpha 2,3 sialyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IEN PC Compatible
OPERATING SESTEM: PC-DOS/MS-DOS
OFFWARE: PERCENTE Release #1.0, Version #1.25
CURRENT APPLICATION BATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Poms, Smith, Lande & Rose: 2029 Century Park Bast, Suite 3800 Los Angeles
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REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/102,385
FILING DATE: AUGUST 4, 1993
ATTORNEZ/AGENT INFORMATION:
                                                                                                                                                  Sequence 1, Application US/08446875
Patent No. 5858751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELECHONE: (310) 277-1297
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/4
APPLING DATE: July 12, 1995
CLASSIFICATION: 435
                         LENGTH: 1218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
569 ITTTGCIAAAAA 581
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LENGTH: 1218 base pairs
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ORGANISM: DOP
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                                                                                                       RESULT 5
US-08-446-875-1
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                                                                                                                                                                                                               OBREAL INTEGRATION:
APPLICANT: Powinto, James C.
APPLICANT: Powinto, James C.
APPLICANT: Gillegie, William
APPLICANT: Gillegie, William
APPLICANT: Weath sorger Name I.
APPLICANT: Weathlegie, William
APPLICANT: Weathlegie, William
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TITLEGE FORWATTONT CONSTRUCTION AND STRIBBLES OF SELFUENCE.
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53.9%; Pred, No. 3.2e-06;
Zative 0; Mismatches 89; Indels 0;
                     754 GAIGGAGIITTTBAGBAGGBAACTGGGAAAGGACAGGGGGCA 794
                                                            304 GROGACCICITCCGGGGTGAGACGGCGAGGACGAGAA 844
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COMPUTER: PLAN PC COMPUTED:
OPERATING SETEM: PC-DOS/MS-DOS
OFFWARE: PERCENTE RElease #1.0, Version #1.25
CURRENT APPLICATION PATA:
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2029 Century Park Bast, Suite 3800
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FILING DATE: July 12, 1995
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REPERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION 435
CLASSIFICATION 435
APPLICATION NUMBER: 08/102,185
FILING DATE: Adjust 4, 1993
ATTORNEY/AGENT INCORATION:
NAME: Oldenkamp, David u.
                                                                                                                                              Nacyon 12:08-446-875-15
; Sequence 15, Application US/08446875
· Datent No. 5858751
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TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 15:
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MEDIUM TYPE: Floppy
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es 104; Conserv
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513 CTGCCGGCCCTGCTGGTGGGCAACCTGAAGGAGTCCTAATGGGCC 572
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STRANDEDNESS: doubl
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OPERATING SYSTEM:
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F: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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   453 TGAGATAGATCCACCTGCATTTGGAGAATGAACAATGCCCCCACCAAAGGTTATGA 512
                                    573 TCAGATAGACAGCCAGGACTICGTGCTGAGGATGAACAAGGGCCCCAGGGGGGTTTGA 632
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                                                                        513 AGAAGATGTCGGCCGCATGACCATGATTCGAGTTGTGTCCCCATACCAGCGTTC 565
                                                                                           633 GGCGGAGGAAGGAAGCACCACAATTCGTGTAACCCCGAGAGCTTCC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%; Score 49.8; DB 2; Length 1218;
55.5%; Pred. No. 6.6e-06;
tive 0; Mismatches 77; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCNTION: 91.,1119
OTHER INPORMATION: /product- "porcine Gal Beta 1,3
OTHER INFORMATION: GalNac alpha 2,3 sialyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park Bast, 38th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PISSUE TYPE: liver, submaxillary glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/102,385G
FILING DATE: 04-AUG-1993
                                                                                                                                                                                                                                                           APPLICANT: Paulson, James C.
APPLICANT: Peulson, James C.
APPLICANT: Hen, Xlaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, Milliam
APPLICANT: Kelm, Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                        Sequence 1, Application US/08102385G
Patent No. 5962294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELERAR (310) 277-1297
INFORMATION FOR SEG ID NO: 1:
SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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388 CTGGACTGTGACCTTTGTGCCATAGTGTCAAACTCAGGTCAGATGGTTGGCCAGAAGGTG 447
                         453 TGAGATAGATOGATOCTOCTOCATTTGGAGAATGAACAATGCCCCCACCAAAGGTTATGA 512
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                                                                                                513 AGAAGATGTCGGCCATGACCATGATTCGAGTTGTGTCCCATACCAGCGTTC 565
                                                                                                                                             533 GCCCGACGTCGGGAGCAAGACCACCCACCATTCGTGTACCCCGAGAGCTTCC 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Fitzpatrick, Cella, Harper & Scinto
277 Park Avenue
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,587A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP-333661/1991
APPLICATION NUMBER: JP-091044/1992
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APPLICANE METALDE EXPUSA
APPLICANE METALDE SERVICE
APPLICANE METALDE SERVICE
APPLICANE BROAD NO SSALGOO
APPLICANE BROAD NO SSALGOO
APPLICANE BROAD NO SSALGOO
MUNICANE METALDE NO SSALGOO
MUNICANE SOURCEMENT 3 STATUTE
                                                                                                                                                                                                                                                                                Sequence 1, Application US/07991587A
Patent No. 5384249
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CELL TYPE: histiocytoma cell
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TELEPHONE: 212-758-2400
TELEFAX: 212-758-2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dos 3.3
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 17-12-1991
FILING DATE: 10-04-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lawrence S. Perry
REGISTRATION NUMBER: 31
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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#71 CTGGAGTGTCGTCGTTGTGTGGGAAATGGGCACCGGTTGCGGAACAGGTCGCTG 530
                                 508 TAIGAAGAAGATGICGGCCGCATGACCATGATTCGAGTIGICCCAT 555
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51.2%; Pred. No. 0.18;
tive 0; Mismatches 82; Indels 0
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277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                     3 Sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.5 inch, 1.44mb
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APPLICATION NUMBER: JP-091044/1992
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20-SEP-1994
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16-12-1992
                                                                                                                                                                                                                       Sequence 1, Application US/08309985
Patent No. 5049790
GENERAL INFORMATION:
APPLICANY: Sasaki, Katsutoshi
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sekine, Susumu
APPLICANT: Hanai, No. 5494790uo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NIDERS: 1560
TELECOMONICATION INFORMATION:
TELECOMONICATION 1760-2962
TELECAN 127-796-2962
INFORMATION FOR SEN 201 DNO: 1:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 31,865
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hangl, No. 549479
APPLICANT: Hasequa, Mamoru
TITLE OF INVENTION: 2 3 Si
NUMBER OF SEQUENCES: 7
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 Watanabe, Etsuyo
Nishi, Tatsunari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-12-1991
FILING DATE: 10-04-1992
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 51.2*
Matches 86; Conservative
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ADDRESSEE: Fitzpatric
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MEDIUM TYPE: Diskette
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FILING DATE: 16-12-
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New York
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148 GGAAATGAGATAGATGGATCTTCTTCTGCATTTGGAGAATGAACAATGCCCCACCAAAAGT 507
                     381 TTTCCAACTGCACTGTGACCTTTGTGCCATAGTGTCAAACTCAGGTGAGATGGTTGGCCA 440
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                                                                                                                 591 TACCAGGAGATGTGGCTCCAAGACCACCATACGTCTGTGTATCCT 638
                                                                                       508 TAIGBAGAAGAIGICGGCCGCAIGACCAIGAITCGAGTIGIGICCCAI 555
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2.84; Score 36.6; DB 1: Length 1048;
Best Local Similarity 55.38; Fred, No. 0.14;
Matches 81; Conservative 0; Mismarches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                  APPLICARY: Shuichi FSUJI et al.
TITLE OF INVENTION: Sia 2,30ala 1,401CMAC '2,8-
TITLE OF INVENTION: SIA 2,30ala 1,401CMAC '2,8-
NUMBER OF SEQUENCIS: 4
CORRESPONDENCE ADDRESS:
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1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 5.1+ (ASCII)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                Sequence 4, Application US/08626994A
Patent No. 5798244
GENERAL INFORMATION:
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MEDIUM TYPE: 1.44 diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: April 3, 1996
CLASSIFICATION: 435
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STRANDEDNESS: not relevant
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TELEPAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 4:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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U.S.A.
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472 AGAGGCTTTCCACAAAGATCTTGGAAGGAAAACCA 506

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82; Indels

388 CFGGACTGFGACCTFFGTGCCATAGFGTCAAACFCAGGTCAGATGGTTGGCCAGAAGGTG 447

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381 TTIGCAACTGGACTGTGACCTTTGTGCCATAGTGTCTAACTCAGGTCAGATGGTTGGCCA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Shinciph 150J1 et al., ASICHAC 2,8-
ITIL OF INVENTION: SIAVITANISFERASE
ITILE OF INVENTION: STAVITRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 CHANGGITATGAAGAAGATGICGGCCGCATGACCA 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greenblum & Bernstein, P.L.C.
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1+ (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,9948
FILING DATE: April 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/957,742 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 77469/1995
FILING DATE: APRIL 3, 1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 6017743
                                                                                                                                                                                                                                                          MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
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COMPUTER: IBM PC competible
OPERATING SYSTEM: NS-DOS
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EDNESS: not relevant
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MEDIUM TYPE: 1.44 dis
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 dl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1660 bases
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US-08-626-994A-2
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                                                                Virginia
                                                                                                               COUNTRY: U.S.A.
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                           Reston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 GAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAATGAACAATGCCCCCCAC 500
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                                                                                                                                                    AGRIRAL INFORMATION:
APPLICATOR: SMALOTH STOUT Et al.
TITLE OF INFURIOR: SIA' 2,30ala 1,401CNRC ' 2,8-
TITLE OF INFURIOR: SIA' 2,30ala 1,401CNRC ' 2,8-
WINDER OF SEQUENCES: 44-
WINDER OF SEQUENCES: 44-
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FREENT NO. 5798244
GREERAL HYDORATION: SALICH FROM C all 1, 4GLORAC 7,8-
TITLE OF UNEWRITCHO: SLAIN 7,94848788048
TITLE OF INVERTION: SLAINTHANSERBASE
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ADDRESSRE: Greenblum & Bernstein, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                  OURBERGEONDERCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION NORTH.
FILING DATE: APRLI 3, 1995
APPLICATION NUMBER: JP 77469/1995
APPLICATION NUMBER: JP 3, 1995
APPLI
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US-08-957-742-4
; Sequence 4, Application US/08957742
; Patent No. 6017743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
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TELECOMNUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,094
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TYPE: nucleic acid
STRANDEDNESS: not relevant
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NEDIUM TYPE: 1.44 di
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CLASSIFICATION: 435
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US-08-957-742-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virginia
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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MADON ILLING DATE: 1957-11-1-1
FRIDE STELLONION NOBER: 60,066710
FRIDE STELLONION NOBER: 60,05710
FRIDE STELLONION NOBER: 60,07545
FRIDE STELLONION NOBER: 60,07545
FRIDE STELLONION NOBER: 61,07541
FRIDE STELLONION NOBER: 61,07510
FRIDE STELLONION NOBER: 61,07510
                        PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
                                                                                          APPLICATION NUMBER: 60/065311
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
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PILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-66-02
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PRIOR FILING DATE: 1998-66-02
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PRIOR APPLICATION NUMBER: 60/088025
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
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PRIOR APPLICATION NUMBER: 60/088167
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PRIOR APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/08655
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PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/08824
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FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-12
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PRIOR APPLICATION NUMBER: 60/08940
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FILING DATE: 1998-06-05
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                                                                     ILING DATE: 1997-11-7
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36.6; DB 3; Length 1660;
Pred. No. 0.19;
0: Mismatches 74; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 CARAGGITATGRAGAGGIGGCGGCGCGCATGACCA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        656 AGAGGCTTTCCACAAGATGTTGGAAGGAAAACCA 690
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CURRENT FILING DATE: 2001-11-14
                APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1396
APPLICATION NUMBER: 2F 7469/1995
FILING DATE: April 3, 1395
ATTORNEY/AGENF INFORMATION:
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Patent No. 6478825
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Goddwark, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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PRIOR FILING DATE: 1997-06-16
                                                                                                                               NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEFAL (703) 716-1191
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            not relevant
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%;
Best Local Similarity 52.3%;
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                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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Paoni, Nicholas F.
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Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Conservative
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Botstein, David
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               LENGTH: 1660 bases
TYPE: nucleic acid
STRANDEDNESS: not r
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US-08-957-742-2
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US-09-996-243-346
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APPLICANT CHARGE INTERPRETATION OF A SELECTION OF A SELEC
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Pred. No. 0.53;
0; Mismatches 54; Indels 0
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CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
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PRIOR FILIND DARE: 1990-06.30
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PRIOR FILING DATE: 1999-03-30
PRIOR PRILICATION MERSES 66/199863
PRIOR PLILAGO MARCE 13991-06-26
PRIOR PRILIAGO MARCE 13991-06-26
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Patent No. 6476208
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Matches 68; Conservative (
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REGISTRATION NUMBER: 60/09599
REGISTRATION NUMBER: 60/095600
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PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
         FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
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Wed Sep 17 16:37:29 2003

SEQ ID NO 1

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LOCATION: 170810
OTHER INFORMATION: 99-16100-147 : polymorphic base A or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIHER INFORMATION: 99-24656-260 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THER INFORMATION: 99-24639-163 : polymorphic base A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 99-24634-108 : polymorphic base A or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 99-7652-162 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: exon z

OTHER INFORMATION: exon z

OCATION: 187091. 24991

SMERTER ADMILLON: Frequilatory region

SMERTER ADMILLON: Frequilatory region

COCATION: 18116

SMERTER ADMILLON: Frequilatory region

COCATION: 18116

SMERTER ADMILLON: POST943-130 : polymorphic base G or
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RAMAZ/KET: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JTHER INFORMATION: 8-128-33 : polymorphic base C or T AMAR/KE: allele (OCATION: 95396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 24046..241153
OTHER INFORMATION: exon WAME/KEY: exon
LOCATION: 241072..241291
OTHER INFORMATION: exon X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME, KEY: exon
LOCATION: 217671..217764
STHER INFORMATION: exon VI
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LOCATION: 238715..238919
OTHER INFORMATION: exon V3
                                                                                                                                                                                                                                                         OTHER INFORMATION: exon S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THER INFORMATION: exon V2
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OTHER INFORMATION: exon W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIRECTINGEMENTION: exon U
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LOCATION: 244353..244561
OTHER INFORMATION: exon Y
                                                                                                         THER INFORMATION: exon S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION: 216836.,216994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INPORMATION: exon V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION: 216836.,217077
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LOCATION: 227655..227736
                                                                                                                                                         NAME/KEY: exon
                                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 214676..214793
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 215702..215746
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                                               201123..201234
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LOCATION: 21672
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LOCATION: 107281
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LOCATION: 160640
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LOCATION: 160876
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         NAME/KEY: exon
LOCATION: 2011
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APPLICANT SURVEY SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVICANT SERVIC
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1146849 GATTGTTGTTGTTGTTGTTGTTACACCTACAGAAAAAAATGTTTTT 116908
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LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/FEE: misc_feeture
LOCAFION: 241686.243685
TREE INCOMMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KET: misc_feature
LOCATION: 290652.,292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 240800.,240993
OTHER INFORMATION: exon MS1 complement g34872 gene
                                                                                                                                                         NAME/KEY: exon
LOCNTION: 240528..241685
COTHER INFORMATION: exon MI complement 934872 gene
FERVIRE:
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LOCATION: 199122.,201122
OTHER INFORMATION: 5'regulatory region
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PRIOR APPLICATION NUMBER: 09/7
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 09/4
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LOCAFION: 292653..292841
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                                                                                                                                                                                                                                                                                                                                                                   NAME / REY: exon
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US-09-679-409-1
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ON: 173358 INFORMATION EY: allele	INFORMATION EX: allele	INFORMATION ET: allele	ON: 200778 INFORMATION EY: allele	202651 ORMATION	202679 SRMATION	EY: Allele ON: 203378 INFORMATION	11el 24.13 GATE	CDN: 204605 INFORMATION:	ON: 204934 INFORMATION	ON: 205206 INFORMATION	ON: 205329 INFORMATION	ON: 206064 INFORMATION	EY: allele ON: 206545 TNEORMATION:	allele 207313	INFORMATION: KEY: allele	RIL	ION: 208950 INFORMATION: KEY: allele	ION: 209123 INFORMATION:	ION: 209631 INFORMATION:	INFORMATION:	ON: 210463 INFORMATION	ON: 210486 INFORMATION	ON: 210583 INFORMATION	ON: 210879 INFORMATION:
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COCATION: OTHER INF	OTHER INF NAME/KET:	OTHER INFO	LOCATION: OTHER INF NAME/KEY:	LOCATION: OTHER INF	LOCATION: OTHER INF	NAME/KEY: LOCATION: OTHER INF	NAME/KEY: LOCATION: OTHER INFO	NAME/KEY: LOCATION: OTHER INFO	LOCATION: OTHER INFO	LOCATION: OTHER INFO	LOCATION: OTHER INFO	NAME/KEI: LOCATION: OFHER INFC	NAME/KET: LOCATION: OTHER THE	NAME/KEY:	NAME/KEY:	OTHER INFO	LOCATION: OTHER INFO NAME/KEY:	IOCATI OTHER	COCATION: OTHER INFO	LOCATION: OTHER INFO	LOCATION: OTHER INFO	LOCATION: OTHER INFO	LOCATION: OTHER INF	LOCATION: OTHER INF
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: variable motif AAAGG or GAAGGAAGGAAGGAAGA Owery Natch 2.7%; Score 35.4; DB 4; Length 319608; Best Local Similarity 45.7%; Pred. No. 16; Natches 91; Conservative 0; Mismarches 91; Indels 0; CACATOR 211355

WARGER 11050

WARGER 11060

WARGER 11060

COUREN WARGER 1106

COUREN WARGER 1016

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                                                                                                                                                                                 New isolated polynucleotide, useful in research, diagnostic or
berapeutic methods, e.g. preventing or treating disorders involving
abscraft protein expression or biological activity.
     Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1294; DB 24; Length 1294; 100.0%; Pred. No. 0;
Liu C, Zhou P, Asundi V, Zhang J, Nehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                        present invention relates to novel human coding sequences
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                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 204; 394pp; English.
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                             Xue AJ, Yang Y,
     Goodrich RW,
                                                                                              WPT: 2002-590824763
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                                                                                                                           N-PSDB; ABP64885
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chondrocyte cell; cell proliferation; cell differentiation; colon; lung; breast; prostate; rectum; cervix; liver; genetic disorder; PCR primer. adrenal: poot;

WO200168848-A2 Homo sapiens

20-SEP-2001

28-FEB-2001; 2001WO-US06520

2000US-187202P 2000US-189320P 2000ffs-191007p 2000US-19104AP 2000ffs-192655p 2000US-193032P 2000US-193053P 2000WO-DS08439 02-MR 2000 03-MR 2000 06-MR 2000 14-MR 2000 11-MR
2000US-194647P 2000US-195975P

2000US-196690P. 2000US-196820P. 2000US-198121P. 2000US-198585P

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2000US-199397p 11-APR-2000; 18-APR-2000; 18-APR-2000; 25-APR-2000; 25-APR-2000; 25-APR-2000;

2000US-199654P. 2000US-201516P. 2000WO-US13705. 2000WO-US14042 2000WO-US14941 25-APR-2000; 03-MAY-2000; 17-MAY-2000; 22-MAY-2000; 30-MAY-2000;

2000WO-US15264 02-JUN-2000; 05-JUN-2000;

2000WO-US20710 2000US-0644848

(GETH) GENENTECH INC

Desnoyers L, . Chen J, Desnoyers L Smith Y, Watanabe CK, 2001-602746/68 Baker KP, Pan J, WPI;

Godowski PJ, Gurney AL;

Shang 2; Goddard A. MI, Wood

of tumours, such as prostate and breast tumours, in mammals and for modulators of the compounds Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of screen S

Claim 2; Fig 535; 774pp; English.

Separace and SMS1953-ASSIG13; represent the maintenance concept and first primary for PRO pulphyperides of the invention. The separaces of the invention can be used to detect the presence of a the university of the properties of the invention of the use of the invention of the use of the invention in a manual by of Collist from the maintain and a control membry for present cell, askeding a higher term than a minimal and a control membry for present cell, askeding a higher term of cells of the cells of the cells of the cells of the cells of the cells of the cells of the cells of the cells and the cells of the cells and the cells and the cells are presented to the cells of the cells and the cells are cells and the cells are cells and the cells are cells and the cells are cells and the cells are cells and the cells are cells and the cells are cells and the cells are cells are cells are cells are cells and the cells are cells

The polypeptides can be used to gitalizate numents exessis factor; (TWB pights "sidises" from human holoco, when contracted with it. A genetic pightspetide can be used to satisfact the profilestor of differentiation of chancomorphic only. Prespectation of many perspectation of the properties on the used to detectine the presence of tunors and also sassophility to tunor development particularly stead of the present in the present of qoats and rabbits but are preferably human. 88888888888888

Sequence 1106 BP: 325 A: 226 C: 260 G: 295 T: 0 other:

44 TOGATOTISCOGGAATGINGGCTTGGAGAGGTCTTGCCGTGGTACTACCAGCTTCCAGCCTTGAGCGCT Gaps ö Score 743.4; DB 22; Length 1106; Pred. No. 4.68-233; Indels 0: Mismatches 57.48; Conservative

TGGATCTGCGGGAA/TGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCC

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CCATGGCCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCC TITICCEGCEGCEGCECCTCTCEAARGEAAGTGAATTTCCCAFFGCTACTAAACTGCT

99 224

284 TIGGACAACCFGGTACAAAGTGGATACCATTCTCCTACACATACAGGCGGCCCCTTCGAA

300

463 420 523 480 583 540 9 703 999

241 TIGGACAACCTGGTACAAAGTGGATACCAYYCICCTACACATACAGGGGGCCCCTTGGAA

464 GATOCTCCTGCATTTGGAGAATGAACAATGCCCCACCAAAGGTTATGAAGAATGTCG

524 GOCGCATGACCATGATTCGAGTTGTGTCCCATACCAGCGTTCCTCTTTGCTAAAAACC 541 CTGATTATTTTTCAAGGAAGCGAATACTACTTTTATGTTATTTGGGGACCTTTCCGCA

704 ATCCGAATGCCCAAATATACGTGACCACAGAGAGCGCAYGAGTTACYGTGATGTGTT 763 544 ATATGAGGAAAGATGGCAATGGCATCGTTTAQAACATGTTGAAAAAGACAGTTGGTATGT

TTAAGAAGGAAACTGGGAAGGACAG 788 TEAGRAGGRACTGGGRAGGCACAG 164

RESULT 3

ACA57950 standard: CDNA: 1206 BP ACA57950 ID ACA5

980S-07745 980S-07745 980S-07764 980S-07764	98US-078939P. 98US-079664P. 98US-079786P. 98US-080107P.	98US-080327P. 98US-080333P. 98US-081049P.	98US-081070P.	98US-081838F.	98US-082704P. 98US-082797P. 98US-083322P.	98US-083495P. 98US-083496P. 98US-083499P.	98US-084414P.	98US-084640P. 98US-084640P. 98US-084643P.			98US-086486P. 98US-086486P. 98US-087098P.			98US-088028P. 98US-088029P.						98US-088825P.		98US-088876P. 98US-089090P.	98US-089512P.	9805-089538P.	98US-089653P. 98US-089908P.
10-MAR-1998; 11-MAR-1998; 11-MAR-1998; 20-MAR-1998;	20-MAR-1998; 27-MAR-1998; 27-MAR-1998; 31-MAR-1998; 31-MAR-1998;	01-APR-1998; 01-APR-1998; 08-APR-1998;	08-APR-1998; 09-APR-1998;	21-APR-1998; 21-APR-1998; 21-APR-1998;	22-APR-1998; 22-APR-1998; 28-APR-1998;	29-APR-1998, 29-APR-1998; 29-APR-1998; 29-APR-1998;	05-MAY-1998; 06-MAY-1998;	07-MAY-1998; 07-MAY-1998; 07-MAY-1998;	15-MAY-1998; 15-MAY-1998; 15-MAY-1998;	15-MAY-1998; 18-MAY-1998;	22-MAY-1998; 22-MAY-1998; 28-MAY-1998;	28-MAY-1998; 02-JUN-1998;	03-JUN-1998; 03-JUN-1998; 04-JUN-1998;	04-JUN-1998; 04-JUN-1998;	04-JUN-1998;	05-JUN-1998;	09-JUN-1998;	10-JUN-1998;	10-JUN-1998; 10-JUN-1998;	10-JUN-1998;	11-JUN-1998; 11-JUN-1998;	11-JUN-1998; 12-JUN-1998;	16-JUN-1998;	17-JUN-1998; 17-JUN-1998;	17-JUN-1998;
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	Human; PRO; secreted; transsembrane; cytostatic; TRF-slpha; blood; gene; different mecras Renora trapha release o'bodirocyte cell; proliferation; esternitation; tumour; gene flatepy; ss.			2002US-0187600.	98NO-US19330. 98NO-US1141. 98NO-US25104.	99NO-18050/28. 99NO-18050/28. 99NO-18127.25.2	21090. 220091.	99MO-1928b51. 99MO-1831574. 2000MO-1800219.	2000MO-TSS4.34. 2200MO-TSS4.3. 270 MON-TSS4.3.	505004. 05601.	2000W0-US00841. 2000W0-US00884. 2000W0-US004839.	2000MO-US13705. 22000MO-US1314042.	.2000MO-1515.544. 2000MO-1515.544.	2000Wo-U52328. 2000Wo-U523052. 5001Wo-TES3652.	2000m0-1834956. 2001m0-US06520.	S17800. S19692.	2001M0-US21046. 2001M0-US2173S. 2007M0-US2173S.	522.63P. 522.63P.	22.400F. 34.86F.	970g-063120P. 970g-063121P.	63540P. 63541P.	3544P. 27364P.	33870P.	74103F. 11 6120F.	6466P. 56772P.

09 284 TROPOLANCITOSTRO, DARANTO CATALOGO CONTINUES 345	164 GANCHOCTROANTIGOAGNATOANCOCCOCCAAAGNTTATTAAAAGNAGATTOOTTAAAAAAAAAAAAAAA	0	13 86	cartilage discarding appears. US2003036156-	TO THE TOTAL COURSE AND THE TO
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2000WD-US00219- 2000WD-US04341. 2000WD-US04342. 2000WD-US04414. 2000WD-US05601. 2000WD-US05601. 2000WD-US05894. 2000WD-US0884. 2000WD-US0884. 2000WD-US0843.	00000000000000000000000000000000000000	9 10 10 10 10 10 10 10 10 10 10 10 10 10
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7.64 TEXAGNAGRANCOGRAGO 786 	ABNORD 5 ABNOR952 D. ABNO8922 standard; CDNN, 1106 BP. AC ARNO8922;	20-MAY-2003 (first entry)	Movel human secreted and transmembrane protein PRO7177 cDNA.	Buman, secreted protein; transmembrane protein; oytostatio; gene Therapy, TRPA-Appida, Albah, Galdocoyte attainator; tumour; adtent tumour; noter tumour; occor tumour; broast tumour; testal tumour; cervical tumour; testal tumour; servical tumour; iss.	Homo saplens.	US2003036157-A1.		ñ	07-0CT-1998; 98M0-1021141. 01-0EC-1998; 98M0-1025108. 08-MMD-1999; 98M0-1056078		11 - 887 - 9599 9 9980 - 1982 0 93. 10 - 887 - 9599 9 9980 - 1982 0 91. 10 - 1987 - 9599 9 9980 - 1982 0 91.	05-2AN-2010; 2010W0-2800219. 18-FEB-2000; 2010W0-080434. 18-FEB-2000; 2010W0-0806434. 22-FEB-2000; 2010W0-0806444.	24 - FEB 2000 / 2000mm - 15985-900 d. - 24 - 2500 / 2000m - 15905 d. 1 25 - PAR 2000 / 2000m - 15905 d. 1 25 - 2500 / 2000m - 15905 d. 1	50 - NAR-2000, 2000/990- 1780/45.9. 52 - NAY-2000, 2000/990- 168.3.7.6. 52 - NAY-2000, 2000/990- 168.3.7.6. 53 - NAY-2000, 2000/990- 168.3.4.1.	20 - UNIX - 2000 2000		2000		24.0021.1997; 9782-0631.200. 24.0021.1997; 9782-0631.200. 26.0021.1997; 9782-06314. 28.0021.1997; 9788-06344.
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57.48; Socze 743.4; DB 25; Length 1106; Yes Licoal Similarity 99:91; Pred, No. 4.6e-233; Langth 1106; Pred, No. 4.6e-233; Lindels 0; Gaps Dhes 744; Conservative 0; Mismatches 1; Indels 0; Gaps

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Homo sapiens. US2003027280-A1 06-FEB-2003.	16-SEP-1998; 07-0CT-1998; 01-DEC-1998; 08-MAR-1999; 14-MAY-1999;	02-70X-1999; 01-SEP-1999; 15-SEP-1999; 01-DRC-1999; 30-DEC-1999; 30-DEC-1999; 05-7AN-2000; 18-FKB-2000;	18-FBS-2000; 22-FBS-2000; 24-FBS-2000; 02-NAR-2000; 02-NAR-2000; 15-NAR-2000; 30-MAR-2000; 17-NAR-2000;	22-MAY-22000 30-MAY-22000 28-JUL-2000; 24-AUG-2000; 08-NOV-2000; 01-DEC-2000; 20-DEC-2000; 28-FEB-2001;	01-JUN-2001; 20-JUN-2001; 29-JUN-2001; 09-JUL-2001; 18-SEP-1997; 18-SEP-1997; 11-0CT-1997; 24-CCT-1997; 24-CCT-1997; 24-CCT-1997;	000000000000000000000000000000000000000	
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643 57.4%; Score 743.4; DB 25; Length 1106; 99.9%; Pred. No. 4.6e-233; Sequence 1106 BP; 325 A; 226 C; 260 G; 295 T; 0 other; 0; Mismatches Claim 2; Fig 535; 701pp; English. Query Match 57.4%; Best Local Similarity 99.9%; fatches 744; Conservative 284 5 ŏ 셤 ò a 셤 ò e ä ò qq ö 문 ö 8 ò a ŏ 8 à Baker KP, Chen J, Desnoyers L, Goddard A, Godowski FJ, Gurney AL, Pan J, Smith V, Watanabe CK, Rood WI, Shang 2; 970S-063754P. 970S-063734P. 970S-063709-970S-06311P. 970S-0662120P. 970S-066468P. 541P 970S-069335P. 2000WO-US15264 2000WO-US20710 2000MD-TIS30952 28-FEB-2001; 2001WO-US06520 01-JUN-2001; 2001MO-US17800 20-JUN-2001; 2001MO-US19692 29-JUN-2001; 2001MO-US21066 09-JUL-2001; 2001MO-US21735 97US-059263p 97US-063486P 97US-063540P 066772P 97US-069870P 98US-077632P 980S-07886P 98US-079939P 98US-080107P 98US-080194P 98US-080327P 98US-080333P 98US-081049P 98US-081195P 98US-081838P 98US-082568P 98US-082569P 98US-082704P 98US-082797p 970S-0635-(GETH) GENENTECH INC. WPI; 2003-066893/06 P-PSDB; ABU10777. 22-MAY-2000; 2 30-MAY-2000; 2 02-JUN-2000; 2 28-JUS-2000; 2 24-AUG-2000; 2 08-NOY-2000; 2 01-DEC-2000; 2 20-MAR-1998; 20-MAR-1998; 27-MAR-1998; 17-0CT-1997 21-OCT-1997 24-NOV-1997 DEC-1997 -APR-1998 22-APR-1998; 28-APR-1998; 29-APR-1998; Baker KP,

Novel isolated PRO polypeptides e.g., PRO1079, PR0827, PR0791, PR01131, PR01131, PR01181, PR01181, PR01181, PR01186, PR01186, PR01181, PR01186, PR01181, PR01186, PR01181, PR01186, PR01180, PR0

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                                                                                  "Mature drug metabolising enzyme (DME-17)"
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Ring HE, Hillman JL, Yue H, Azimzai Y, Yao MG, Ga
Nguyen DB, Tang YI, Lai P, Bandwan O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human drug metabolising enzyme (DME-17) cDNA.
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21-JAN-2000; 2000US-0177443.
28-JAN-2000; 2000US-0178574.
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Pred. No. 3.8e-223;
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Shi Y, Choi GH, Fiscella M;
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Wei P, Ebner R, Duan DR,
                                                                                                                                                                              764 TIRAGRAGGAAACTGGGAAGGACAG 788
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P-PSDB; AAE21595.
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Moore PA,
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                                                                                                                                                                                                                                                                            Score 713.8; DB 24; Length 3189;
Pred. No. 5e-223;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                       Sequence 3189 BP; 993 A; 614 C; 624 G; 958 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                    718; Conservative
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immune systems carticovascaix; sepicoment, pastroitestinal, endocrine,
preparancy-risted disorder; constitues enterological, unclimante discose;
inflamantion, alleny, rhematoid erthitis Alzebier's disease;
mentinons disease; softlerhemis presists; sepais; beforeoticus;
disbetes; infection; wound healing; vulnerary, chemotxas; food ddilites
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                                                                                                                                                                                                                             Human secreted protein-encoding dene 1 cDNA clone HE9PR39, SEC ID NO:1.
                                                                                                                                                                                                                                                                                        secreted protein; proliferative disorder; cancer; tumour; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating and preventing cancer, immune disorders (e.g. Addison's disease, and allergies), and cardiovascular disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birse CE, Soppet DR, Olsen
Shi Y, Chol GE, Riscella M;
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100..189
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Duan DR,
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100..1017
                                   AAD34106 standard; cDNA; 3189 BP.
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Moore PA,
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185 GAAAGTCTGTGTGTGTGTGAGCTTCATAGCGTTCCTTTTCCTGCTGGTTGTGCGTC 244

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GGGGGCCCCCTGCTCCGGTGGCAGGGCCGGCGGAGCGCCATGGCCTGCATGCCTGCATCCTGAAGA 61

355 TGBAGACACAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAACTCAG 424 30.2 GRONGREGOFFIGURE CONTRACTOR STATEMENT CONTRACTOR CONTRACTOR SET 35.1 485 TGAACAATGCCCCCCCACCAAGGTTATGAAGAAGATGTCGGCCCCCATGACGATGATTCGAG 544

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245 TIGTARATGAAGTGAATTTGCCATTGCTACTAAACTGCTTTGGACAACCTGGTACAAAGT

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                                                                                                    nootropic; neuroprotective;
immunosuppressant; cardiant;
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                                                                                                                                                                                                                            hypertension:
                                                                                                                   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
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                         Human ORFX ORF2033 polynucleotide sequence SEQ ID NO:4065
                                                                                                    antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 3256; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; contraceptive; ss.
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30-MAR-2000, 2000US-0540763
                                                                                                    vulnerary; antipsoriatic;
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Search completed: September 12, 2003, 12:46:49
Job time : 422 secs
562 ACAG 665
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125 GOGCGCCCGCTGCTCGGTGGCAGGAGGCCCGGGGGGCCCCATGCCCTGCATCCTGAAGA 184

50.4%; Score 652.4; DB 21; Length 696; 98.8%; Pred, No. 2.8e-203;

coaquiation; to inhibit thrombosis; and as a contraceptive.

Sequence 696 BP: 191 A: 148 C; 175 G; 179 T; 3 other;

0; Gaps

8; Indels

0; Mismatches

98.86;

Matches 656; Conservative

Best Local Similarity

Query Match

785 ACAG 788

17 763-4 57-4 1106 12 08-10-174-589-515 Sequence 555, 18 763-6 77-4 1106 12 08-10-174-515-515 Sequence 555, 18 763-6 77-4 1106 12 08-10-17-716-515 Sequence 555, 18 763-6 77-4 1106 12 08-10-17-716-515 Sequence 555, 18 76-716-716-716-716-716-716-716-716-716-7	743.4 57.4 1106 12 181-727-784-555 sequence 743.4 57.4 1106 12 181-775-786-555 sequence 743.4 57.4 1106 12 181-775-486-555 sequence 743.4 57.4 1106 12 181-775-489-555 sequence 743.4 57.4 1106 12 181-775-785-555 sequence 743.4 57.4 1106 12 181-775-785-555 sequence 743.4 57.4 1106 12 181-775-785-555 sequence 743.4 57.4 1106 12 181-775-785-785	7.13.4 57.4 1106 12 18-10-776-225-32 Sequence 7.13.4 57.4 1106 12 18-10-776-225-33 Sequence 7.13.4 57.4 1106 12 18-10-776-285-33 Sequence 7.13.4 57.4 57.4 57.4 57.4 57.4 57.4 57.4 57	743.4 57.4 1106 13 US-10-032-568-535 Segrence 743.4 57.4 1106 14 US-10-032-565-555 Segrence 743.4 57.4 1106 14 US-10-10-10-56-555 Segrence 743.4 57.4 1106 14 US-10-10-10-56-555 Segrence	743.4 57.4 1106 14 US-10-173-706-535 743.4 57.4 1106 14 US-10-175-738-35 743.4 57.4 1106 14 US-10-175-738-35 74.4 57.4 1106 14 US-10-175-738-35	555 No. 10520048442AB No. 10520044442AB No. 10520044442AB No. 10520044442AB No. 1052004444AB No. 1052004444AB No. 105204844AB No. 10520484AB No. 10520484BB No. 1052048AB No. 10520484BB No. 10520484BB No. 1052	A PRILIAME TO A CALLERY OF THE TOTAL THE STATE OF THE STA	FILE PERSENCE PARINCE TO SELECTION OF THE PERSENCE PARINCE TO SELECTION OF THE PERSENCE PARINCE TO SELECTION OF THE PERSENCE PARINCE TO SELECTION OF THE PERSENCE	PRICE PATTOR PAT
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Composen Ltd. OM modalc - muckets search, washes or modal Bun no.	(Vilhort alignments) (Vilhort	Scoring table: IDSMITH_MNC GREPO 100: Gapert 1.0 Searched: 137420 segp; 113397814 residues Toral number of bits satisfytue cheen parameters: 756840	eg length: 0 eq length: 2000000000	Post-processing: Maximum Match 10% Match 10% Listing List 65 summaries	Published Publ	Pred. No. is the number of results predicted by chance to have a score greater this or egal to the score of the result being printed, and is derived by analysis of the score of their publich.	Regult Oper Description No. Score Match Leagth DB ID Description	1 713.4 57.4 1106 12 (17.11) 110-17-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 731.4 57.4 1106 12 (17.11) 110-17-1518 Sequence 555, App. 17.1 110-17-17-17-17-17-17-17-17-17-17-17-17-17-

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PRIOR APPLIACATION WINNERS. 660/053544
Remaining Frior Application data removed - See File Wrapper or PALM.
                                                                                                                                                                     Query Match 57.4%; Score 743.4; DB 12; Length 1106; Best Local Similarity 99.9%; Pred. No. 4.1e-237; Matches 74; Conservative 0; Mismatches 1; Indels 0;
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Publication No. US20030153036A1
GENERAL INFORMATION:
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                                                                                                                         ORGANISM: Homo Sapien
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Al Similarity 99.9; Pred. No. 4.1e-237; 744; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/187,749
CURRENT FILING DATE: 2002-07-01
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PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                Smith, Victoria
Watanabe, Colin
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Zhang, Zemin
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US-10-187-749-535
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Best Local Similarity
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61 CCAGGACTGCCCCTGACCCAGGCGCCCCCTGCTCGGTGGCAGGAGGGCCCGGCGGAGCG 120
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Publication No. US20030157635A1
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Gurney, Austin L.
Pan, James
Smith, Victoria
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              ORGANISM: Homo Sapien
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                                                                              164 GATCCTCCTGCATTTGGAGAATGAACAATGCCCCCCACCAAAGGTTAIGAAGAAGATGTCG 523
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Publication No. US20030153037A1
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FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063541
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PRIOR FILING DATE: 2002-01-15
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PRIOR APPLICATION NUMBER: 60/063544
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
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99.9%; Pred. No. 4.1e-237;
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NUMBER OF SEQ ID NOS: 612
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                                                                         Sequence 535, Application US/10196747
Publication No. US20030162250A1
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CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2002-07-16
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GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
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Matches 744; Conservative
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CURRENT FILLING DATE: 2002-06-17
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Watanabe, Colin R.
Wood, William I.
Goddard, Audrey
Godowski, Paul J
Gurney, Austin I.
Pan, James
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Publication No. US20030166107A1
GENERAL INFORMATION:
                                                                                                                                                                                                99.98;
                                                                                                                                                                                                                   Local Similarity 99.9
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                                                                                                                        Homo Sapien
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                   SB4 CIGATIAITITITICAAGGAAGCGAAIACIACIATITIGIGITAITITIGGGGACCITITICGCA 643
                                                                  341 CIGATTATTITICAAGGAAGCGAATACTACTATTAIGTTATTIGGGGACCTITCCGCA 600
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                                                                                                                                               704 ATCCGAATGCCCAAATATACGTGACCACAGAGAAGCGCATGAGTTACTGTGATGGAGTTT 763
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THILL OF INTERTION: SEXEME DAM NUMBERSHAMEN POLITEPTIDES AND WICLEUR.
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Pred. No. 4.1e-237;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                      764 TTAAGAAGGAAACTGGGAAGGACAG 788
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Publication No. US20030166109Al
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 744; Conservative
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Godowski, Paul J.
Gurney, Austin I.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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APPLICANT: Chen, Jian
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LENGTH: 1106
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CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ IN NOS: 612
                       TTARGARGAACTGGGAAGGACAG 745
764 TTAAGAAGGAAACTGGGAAGGACAG 788
                                                                                                                                                                  Sequence 535, Application US/10173698
Publication No. US20030166108A1
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
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US-10-173-698-535
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                                                                                                                                                                                                                                                                      Chen, Jian
                                                                                                                                                                                                                      GENERAL INFORMATION:
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121 CCATGGCTGCATCCTGAAGAGAAAGTCTGTGAATGCTGTGAGCTTCATAGCAGCTTCC 180
                                                      TITICCIGCIGGIIGICOTCICIANAIGAAGIGAAIITCCCAITGCIACTAAACIGCI 283
                                                                                           TITICCIGCIGGITGIGCGICTIGIBBATGAAGIGAATTICCCATIGCTACTAAACTGCT 240
                                                                                                                                TIGGACAACCIGGIACAAAGIGGAIACCAITCICCIACACAIACAGGGGGGCCCCITCGAA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                 524 GCCGCATGACCATGATTCGAGTTGTGTCCATACCAGCGTTCCTCTTTTGCTAAAAACC 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ACIDS ENCODING THE SAME PILE REPERENCE: P3430RIC39
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CURRENT FILING DATE: 2002-06-18
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; Publication No. US20030166111A1
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin E.
Pan, Jamés
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Watanabe, Colin K.
Wood, William I.
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APPLICANT: Baker, Kevin P.
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US-10-174-569-535
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                                                              164 GATCCICCIGCATTINGAGAATGAACAAIGCCCCCCCCCAAAGGTTAIGAAGAAGAIGTOG 523
                                                                                                                                       GCCGCATGACCATGATTCGAGTTGTGTCCCATACCAGCGTTCCTCTTTGCTAAAAAACC 583
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   CICACTAIGGATACATAAATGIGAAGACACAAGAGCCITIGCAACTGGACTGIGACCITT 360
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TYTILE OF TANGNYILON: SECRETED AND TRANSMEMBRANE FOLTPEPTIDES AND NUCLETIC
FYTHE OF TANGNYILON: ACADIS ENCODING THE SAME
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Pred. No. 4.1e-237;
0; Mismatches 1; Indels 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/173,707
CURRENT FILING DATE: 2002-06-17
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Publication No. US20030166110A1
GENERAL INFORMATION:
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin E.
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APFLICANT: Chen, Jian
APFLICANT: Despoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddord, Audrey
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Matches 744; Conservative
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      TITLE OF HUMBRION SCREENED AND PRANSMERGRAME POLITIESTIES AND MOLLETCH THILL OF HUMBRION, ACTUE ENCOUNTS THE SAME PROPERTIES AND MOLLETCH THILL OF HUMBRION, ACTUE ENCOUNTS THE SAME PROPERTIES AND MOLLETCH CONTRACT STATEMENT SHAPE AND MORROW REPLICATION MORROWS. US. 070,774,583
PELIC SPIRITURE MORROWS. 073 - 588 FILE WRAPPER OF PAIR
WOMER DE SROU IN DAYS. 612 - 588 FILE WRAPPER OF PAIR
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Job time : 366 secs
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Score 743.4; DB 12; Length 1106;
Pred. No. 4.1e-237;
0; Mismatches 1; Indels 0;
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Publication No. US20030166112A1
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Smith,Victoria
Watenebe,Colin K.
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Godowski, Paul J.
Gurney, Austin L.
                                      744; Conservative
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   Query Match
Best Local Similarity
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GenCore Version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using aw model. Run on: Suprember 12, 2003, 12:8128; Search time 316 Seconds [0725:85] Million of eall updates/sec	Title: 08-09-714-936-218 CS-09-714-936-218 CS-09-714-936-218 CS-05-714-936-218 CS-05-714-936-936-938 CS-05-714-936-938 C	Socring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	Searched: 22781392 seqs, 12152238056 residues Total number of bits satisfying chosen marameters: 45562784		Post-processing: Manimum Match On Maximum March 1004 [Astrupt first 45 summartes	Database : 587:-; 1. eq.extbar- 2. eq.extbar- 3. eq.extbar- 4. eq.extbar- 5. eq.extbar- 6. eq.extbar- 7. eq.extbar-	F connector)	Dr.	13: 90_set: 1. 14: 90_set: 1. 15: em_ercen 16: non-ercen	13: en_cyst_hum:* 18: en_cyst_hum:* 19: en_cyst_hum:* 19: en_cyst_hum:* 10: en_cyst_		25 on the state of	29: ph_ges2:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result helps printed, score greater than or equal to the score of the result helps printed.	and is del	Nearlit

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contact RRD (LoneWested de) for further information. Seq primer:
MIJS, Primer sequence: GGTGTNAANGONGGCOMST.
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Contact: Ina Rolfs
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/clone_lib="NIH_MGC_147"
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High quality sequence stop: 523.
Location/Qualifiers
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AGENCOURT_6507757 NHLNGC_125 Homo sapiens cDNA clone IMAGE:5724478
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Mammalla; Burberia; Primeres; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1088)
                                                                                                                            /note="Vector: pcDMA3.1; Site_1: BCORI; Site_2: NotI; Library made with RRA pooled from multiple tissues fulluting librar, lung hypothalamus, pituitary, and placenta/endometrium."
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National Institutes of Health, Wammalian Gene Collection (MGC)
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                                         /lab_host-"DH10B"
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"tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                         166 9
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                                                                                                                                                                                                                                                                                                      GTCGGCCGCATGACCATGATTCGAGTTGTGTCCCAAACCAGCGTTCCTCTTTGCTAAAA 579
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Nammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus
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TITATENG-COR-1-12-0-UI:1 MILBARP-FWO Mus musculus CONA clone
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Location/Qualifiers
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This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                   Bukarjota; Metazoa, Chordata; Craniata; Vertebrata; Bitaleostomi; Mommalia; Eutherata; Solentasi Soluropnathi; Muridee; Muzinae; Muz. 1 (Bases I to 766) and 1000, anh gov. Nat. Mod. Pty./Mog.not. 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 10
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Contact: Robert Strausberg, Ph.D.
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Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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directionally into pYX-Asc vector.
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Please Yist our web site (http://geomes.geo.riken.go.jp) for Laboratory for Genome Exploration Research Group, RIKBN Genomic Sciences Center(GSC), Yokohama Institute First Fir 635 bp mRNA linear EST 26-OCT BB659263 RIKEM full-length enriched, 13 days embryo heart Mus museculus CDNA clone D330028F02 5', mRNA sequence. 608 GOCTATCCACATGCCCACACCTGACCACACAGAGCAGCAGCAGTGACTCACT 659 700 AICTAICCGAAIGCCCAAAIAIACGIGACCACAGAGAGGGGCAIGAGIIACI 751 Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNR IKEN Mouse ESTs (Arakawa,T., et al. 2001) /organism="Mus musculus" /db_xref="taxon:10090" Unpublished Contact: Yoshihide Hayashizaki /tissue_type="heart" Location/Qualifiers 1. .635 /clone="D330028F02" Mus musculus (house mouse) /mol_type="mRNA" 88659263.1 GI:16493085 e mouse tissues. further details EST DEFINITION DRGANISM TITLE JOURNAL COMMENT ACCESSION REFERENCE BB659263 KEYWORDS g ò mannaka, I. Kipawa, R. Kondo, S. Satto, T. Silangawa, A. Anawa K. Pakwas, S. Bara, I. Dolyak, Kenalai, Silangawa, A. Anawa, I. Yang Mayanataki, Y. Kenalai, Silantak, A. Anakwa, T. Mayaliga di 1932 mana caba noma chramasama, J. Struct. Masa visit un 1932 mana caba noma chramasama, J. Struct. Lincher detailou: web site (http://penne.gac.riken.go.jp) for transcribtuse and subsequently entitled greener.

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Homo sapiens (human)
Enkaryota Metazoa; Chordata; Cranista; Vertebrata; Buteleostomi; Mammalia;
Butherita; Primites; Catarrinin; Hominidae; Homo.
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Newes H.W., Well B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
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Close from 5' Research Obscalars chooses Malaysis, German Cancer
Research Center (RFF2), EMAI a **Membrid#Eff2-heidslprey; de,
sequenced by EMI. (Entropean Molecular Biology Liboratories,
Heidelbery/Germanny) within the GMA, sequencing consortium of
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This cone (NFESPGEGORISTA) is available at the REPD in Berlin.
Please contact the REPD: Ressourcemantrum, Heubnerveg 6,
14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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98.8%; Pred. No. 6.3e-82;
                                                                                                                                                                 Last updated, Version 1)
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0; Mismatches 102;
'dev_stage="13 days embryo"
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Institutes of Ballh (MIM) Building 49, Room 4082 49 Convent Drive
NSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully
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(TSEA) system—184-tornat esquencing population with 384 anitorpilating sequences; esquencing population (10, 1597-171) (2000)
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11-7-28 Gebrid: Orbo, Faurumi-Ku, Kokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                           Mammalia; Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
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prepare mouse tissues.
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William J Pavan, Stacie Loftus, and
Mus musculus (house mouse)
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                                                                       ORGANISM
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